

Example Fig 1b: 64pp: English.

XX The present invention describes a conjugate composition comprising a
XX treatment of HIV-1 or non-HIV-1 Vpr protein conjugated to a therapeutic
XX compound. The conjugate can be used in a method for inhibiting cell
XX proliferation. It can also be used for treating an individual who has a
XX hyperproliferative disease. The HIV-1 Vpr or non-HIV-1 Vpr protein
XX treatment can be used for identifying compounds that inhibit Vpr protein
XX binding to the p6 domain of p55 or to p6 protein. The present sequence
XX represents an HIV protein sequence.

XX Sequence: 96 AA.

Query Match 100.0% Score 519; DB 20; Length 96;
Best Local Similarity 100.0% Prod. No. 6-57;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

07 1 MGADPEGQVDEPYNIMTLELEKKNVAFPRPWLSLQHYETGDTWVEAL 60
10 1 MEGPDQHPPEYPRWDLKQVDFPRWLSLQHYETGDTWVEAL 60
1b 1 MEGPDQHPPEYPRWDLKQVDFPRWLSLQHYETGDTWVEAL 60

07 61 LRIQGLLFTHPRICVHSRIGILGGRIRNASKS 96
1b 61 LRIQGLLFTHPRICVHSRIGILGGRIRNASKS 96

1b 61 LRIQGLLFTHPRICVHSRIGILGGRIRNASKS 96

RESULT 2

AAW99815 standard: protein: 96 AA.

AAW99815.

07 08-JUN-1999 (first entry)

XX HIV-1 Vpr protein.

XX HIV-1 Vpr protein.

XX HIV-1 Vpr protein.

XX Human immunodeficiency virus type 1.

XX W099412 AL.

XX 25-JUN-1999.

XX 14-AUG-1998; 98W0081690.

XX 14-AUG-1997; 97J080055754.

XX (OYE-) UNIV PENNSYLVANIA.

XX Ayyavoo V, Kibbet Emmons T, Mahalingam S, Patel M;

XX Weimer DB;

XX W01: 1999-181154/15.

XX conjugate composition comprising HIV-1 Vpr protein treatment - used
XX to inhibit cell proliferation and treating hyperproliferative
XX disease.

XX Example Fig 1b: 64pp: English.

XX The present invention describes a conjugate composition comprising a
XX treatment of HIV-1 or non-HIV-1 Vpr protein conjugated to a therapeutic
XX compound. The conjugate can be used in a method for inhibiting cell
XX proliferation. It can also be used for treating an individual who has a
XX hyperproliferative disease. The HIV-1 Vpr or non-HIV-1 Vpr protein
XX treatment can be used for identifying compounds that inhibit Vpr protein
XX binding to the p6 domain of p55 or to p6 protein. The present sequence
XX represents an HIV-1 Vpr protein sequence.

XX Sequence: 96 AA.

Query Match 100.0% Score 519; DB 20; Length 96;

Best Local Similarity 100.0% Prod. No. 6-57;

Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

07 1 MGADPEGQVDEPYNIMTLELEKKNVAFPRPWLSLQHYETGDTWVEAL 60
1b 1 MEGPDQHPPEYPRWDLKQVDFPRWLSLQHYETGDTWVEAL 60

07 61 LRIQGLLFTHPRICVHSRIGILGGRIRNASKS 96
1b 61 LRIQGLLFTHPRICVHSRIGILGGRIRNASKS 96

RESULT 3

AAW99815 standard: protein: 96 AA.

AAW99815.

07 08-JUN-1999 (first entry)

XX HIV Vpr wt protein sequence.

XX HIV: VPR; human immunodeficiency virus; hyperproliferative disease;

XX cell proliferation.

XX Human immunodeficiency virus.

XX W099412 AL.

XX 25-JUN-1999.

XX 14-AUG-1998; 98W0081690.

XX 14-AUG-1997; 97J080055754.

XX (OYE-) UNIV PENNSYLVANIA.

XX Ayyavoo V, Kibbet Emmons T, Mahalingam S, Patel M;

XX Weimer DB;

XX W01: 1999-181154/15.

XX conjugate composition comprising HIV-1 Vpr protein treatment - used
XX to inhibit cell proliferation and treating hyperproliferative
XX disease.

XX Example Fig 1b: 64pp: English.

XX The present invention describes a conjugate composition comprising a
XX treatment of HIV-1 or non-HIV-1 Vpr protein conjugated to a therapeutic
XX compound. The conjugate can be used in a method for inhibiting cell
XX proliferation. It can also be used for treating an individual who has a
XX hyperproliferative disease. The HIV-1 Vpr or non-HIV-1 Vpr protein
XX treatment can be used for identifying compounds that inhibit Vpr protein
XX binding to the p6 domain of p55 or to p6 protein. The present sequence
XX represents an HIV protein sequence.

XX Sequence: 96 AA.

Query Match 95.2% Score 494; DB 20; Length 96;
Best Local Similarity 96.9% Prod. No. 1-54;

Matches 96; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

07 1 MGADPEGQVDEPYNIMTLELEKKNVAFPRPWLSLQHYETGDTWVEAL 60
1b 1 MEGPDQHPPEYPRWDLKQVDFPRWLSLQHYETGDTWVEAL 60

07 61 LRIQGLLFTHPRICVHSRIGILGGRIRNASKS 96
1b 61 LRIQGLLFTHPRICVHSRIGILGGRIRNASKS 96

10 61 trlqqulthfrthstrtdqthrrtnqskss 96

RESULT 4

10 AAW99819 standard: protein: 96 AA.

XX AAW99819:

08-JUN-1999 (first entry)

14 HIV A56P protein sequence.

14 HIV A56P protein sequence.

14 HIV A56P protein sequence.

14 HIV A56P protein sequence.

14 HIV A56P protein sequence.

14 HIV A56P protein sequence.

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14 HIV A56P protein sequence.

14 HIV A56P protein sequence.

14 HIV A56P protein sequence.

XX HIV: Vpr: human immunodeficiency virus: hyperproliferative disease:
cell proliferation.

XX Human immunodeficiency virus.

XX W09909412-A1.

XX 25-FEB-1999.

14-AUG-1998: 98W0-US16890.

14-AUG-1997: 97US-0055754.

(TYPE-) UNIV HINNSTIVARIA.

ATTORNEY V. Klobner Emmanu T. Mahalingam S. Patel M.

W09909412-A1.

Conjugate composition comprising HIV-1 Vpr protein treatment - used

to inhibit cell proliferation, and treating hyperproliferative

diseases.

Example: Fig 1B: 64pp: English.

The present invention describes a conjugate composition comprising a

treatment of HIV-1 or non-HIV-1 Vpr protein conjugated to a therapeutic

compound. The conjugate can be used in a method for inhibiting cell

proliferation. It can also be used for treating an individual who has a

hyperproliferative disease. The HIV-1 Vpr or non-HIV-1 Vpr protein

fragments can be used for identifying compounds that inhibit Vpr protein

binding to the p6 domain of p55 or to p6 protein. The present sequence

represents an HIV protein sequence.

Sequence 96 AA:

Query Match 94.8% Score 488 DB 20 Length 96

Best Local Similarity 95.8% Prod. No. 4.4e-53

Matches 927 Conserved 0 Mismatch 4 Indels 0 Gaps 0

1 MEQAFEDQDQREPMWMTLEEEKNEAVRHPKMLHSLOHYETGPMWVAI 60

61 trlqqulthfrthstrtdqthrrtnqskss 96

61 trlqqulthfrthstrtdqthrrtnqskss 96

61 trlqqulthfrthstrtdqthrrtnqskss 96

61 trlqqulthfrthstrtdqthrrtnqskss 96

61 trlqqulthfrthstrtdqthrrtnqskss 96

61 trlqqulthfrthstrtdqthrrtnqskss 96

61 trlqqulthfrthstrtdqthrrtnqskss 96

61 trlqqulthfrthstrtdqthrrtnqskss 96

61 trlqqulthfrthstrtdqthrrtnqskss 96

61 trlqqulthfrthstrtdqthrrtnqskss 96

61 trlqqulthfrthstrtdqthrrtnqskss 96

50 Sequence 96 AA:

Query Match 94.0% Score 487; DB 20; Length 96;
Best Local Similarity 95.8%; Prod. No. 5,86-53;
Matches 92; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

07 1 MEQATPEQRENTNKTLLLEKNAVHTFWLHSGHITTTGATWVWAL 60
|||||
Db 1 meqpedqrpqpyndkllleeknaevhtfwlshghittdtwtvwal 60
07 61 IRILGQLLFFHFRICRSHKSGILIQDRITNCKSKS 96
|||||
Db 61 irilqqllylfrhcrshsksgilqdrtrncksk 96

RESULT 9

AAW99823
ID AAW99823 standard; protein: 96 AA.

XX AAW99823;

XX 08-JUN-1999 (first entry)

XX HIV 168S protein sequence.

XX HIV-1 Vpr: human immunodeficiency virus; hyperproliferative disease;
cell proliferation.

XX Human immunodeficiency virus

XX W09909412-A1.

XX 25-FEB-1999.

XX 14-AUG-1998; 98WO-081680

XX 14-AUG-1997; 97US-005754.

XX (OYPE-) UNIV PENNSYLVANIA.

XX AAY9909 V. Kieber; Emmons T. Mahalingam S. Patel M;
Weiner DB;

XX WPI: 1999-181154/15

XX Conjugate composition comprising HIV-1 Vpr protein fragment used
to inhibit cell proliferation, and treating hyperproliferative

XX diseases

XX Example; Fig 1b; 64pp; English.

XX The present invention describes a conjugate composition comprising a
fragment of HIV-1 or non-HIV-1 Vpr protein conjugated to a therapeutic
compound. The conjugate can be used in a method for inhibiting cell
proliferation. It can also be used for treating an individual who has a
hyperproliferative disease. The HIV-1 Vpr or non-HIV-1 Vpr protein
fragments can be used for identifying compounds that inhibit Vpr protein
binding to the p5 domain of p55 or to p6 protein. The p5 or p6 sequence
represents an HIV protein sequence.

XX Sequence 96 AA:

Query Match 94.0% Score 487; DB 20; Length 96;

Best Local Similarity 95.8%; Prod. No. 5,86-53;
Matches 92; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

07 1 MEQATPEQRENTNKTLLLEKNAVHTFWLHSGHITTTGATWVWAL 60
|||||

Db 1 meqpedqrpqpyndkllleeknaevhtfwlshghittdtwtvwal 60

07 61 IRILGQLLFFHFRICRSHKSGILIQDRITNCKSKS 96

Db 61 irilqqllylfrhcrshsksgilqdrtrncksk 96

RESULT 10

AAW99825
ID AAW99825 standard; protein: 96 AA.

XX AAW99825;

XX 08-JUN-1999 (first entry)

XX HIV 167Y protein sequence.

XX HIV-1 Vpr: human immunodeficiency virus; hyperproliferative disease;
cell proliferation.

XX Human immunodeficiency virus.

XX W09909412-A1.

XX 25-FEB-1999.

XX 14-AUG-1998; 98WO-081680.

XX 14-AUG-1997; 97US-005754.

XX (OYPE-) UNIV PENNSYLVANIA.

XX AAY9909 V. Kieber; Emmons T. Mahalingam S. Patel M;
Weiner DB;

XX WPI: 1999-181154/15.

XX Conjugate composition comprising HIV-1 Vpr protein fragment used
to inhibit cell proliferation, and treating hyperproliferative

XX diseases

XX Example; Fig 1b; 64pp; English.

XX The present invention describes a conjugate composition comprising a
fragment of HIV-1 or non-HIV-1 Vpr protein conjugated to a therapeutic
compound. The conjugate can be used in a method for inhibiting cell
proliferation. It can also be used for treating an individual who has a
hyperproliferative disease. The HIV-1 Vpr or non-HIV-1 Vpr protein
fragments can be used for identifying compounds that inhibit Vpr protein
binding to the p5 domain of p55 or to p6 protein. The present sequence
represents an HIV protein sequence.

XX Sequence 96 AA:

Query Match 94.0% Score 487; DB 20; Length 96;

Best Local Similarity 95.8%; Prod. No. 5,86-53;
Matches 92; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

07 1 MEQATPEQRENTNKTLLLEKNAVHTFWLHSGHITTTGATWVWAL 60
|||||

Db 1 meqpedqrpqpyndkllleeknaevhtfwlshghittdtwtvwal 60

07 61 IRILGQLLFFHFRICRSHKSGILIQDRITNCKSKS 96
|||||

Db 61 irilqqllylfrhcrshsksgilqdrtrncksk 96

RESULT 11

AAW99826
ID AAW99826 standard; protein: 96 AA.

XX AAW99826;

XX 08-JUN-1999 (first entry)

61. **BRITISHLY IDENTIFICATION OF BRITISH INK** 96
 62. **BRITISHLY IDENTIFICATION OF BRITISH INK** 96
 63. **BRITISHLY IDENTIFICATION OF BRITISH INK** 96

[illegible]

•

[illegible]

|||||
 61 IRIIQQILFIRIICGHSRIGVIRRRANASRS 96

RESULT 4

US-09-700-408 67

Sequence 67, Application US/09700409
 GENERAL INFORMATION:
 APPLICANT: Acad. Ahmed A.
 APPLICANT: Macradia, Jan G.
 APPLICANT: Armaguet, Christian
 TITLE OF INVENTION: VPR AND VPX PROTEINS OF HIV
 NUMBER OF SEQUENCES: 74

CORRESPONDENCE ADDRESS:
 ADDRESS: 400 SEVENTH STREET, N.W.
 CITY: WASHINGTON
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20004

COMPUTER PROGRAM: IBM PC COMPATIBLE
 MEDIUM TYPE: FLOPPY DISK
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09-730,408
 FILING DATE: 25-NOV-1996
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: AU 60902
 FILING DATE: 23-SEP-1995

ATTORNEY, COUNSEL AND AGENT:
 NAME: Holman, John G.
 REGISTRATION NUMBER: 22,769
 REFERENCE NUMBER: 9944, 16858000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-638-6542
 TELEFAX: 202-638-5330
 INFORMATION FOR SEQ ID NO: 67:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 96 amino acids
 TYPE: amino acid
 STRANDNESS:
 IDENTITY: linear
 FEATURE:
 MOLECULE TYPE: peptide
 US-08-700-408-17

Query Match 89.0%, Score 461, DB 11, Length 96
 Best Local Similarity 87.5%, Field No 9, 49

Matches 84: Conservative 7, Mismatches 5, Indels 0, Gaps 0

QY 1 MEOAEPDGPPEPPYNNWITLLELEKNEAVRPPIWLSIQHITYETGTMVEAL 60
 |||||
 DB 1 MEOAEPDGPPEPPYNNWITLLELEKNEAVRPPIWLSIQHITYETGTMVEAL 60
 QY 61 IRIIQQILFIRIICGHSRIGVIRRRANASRS 96
 |||||
 DB 61 IRIIQQILFIRIICGHSRIGVIRRRANASRS 96

RESULT 5

US-09-309-572-19

Sequence 19, Application US/09309572
 GENERAL INFORMATION:
 APPLICANT: HelixBio-Vector Institute
 APPLICANT: Delaporte, Eric
 TITLE OF INVENTION: In Situ Hybridization Probes Pseudotyped with HCMV
 FILE REFERENCE: 950489
 CURRENT APPLICATION NUMBER: US/09-409,572

|||||
 61 IRIIQQILFIRIICGHSRIGVIRRRANASRS 96

RESULT 6

US-09-718-096-19

Sequence 19, Application US/09718096
 GENERAL INFORMATION:
 APPLICANT: Von Loer, Melke-Dorthea
 TITLE OF INVENTION: RETROVIRAL HYBRID VECTORS PSEUDOTYPED WITH HCMV
 FILE REFERENCE: 95-195
 REGISTRATION NUMBER: 2003-11-22
 PRIOR APPLICATION NUMBER: DE 19856463 5
 PRIOR FILING DATE: 1998-11-26
 PRIOR FILING DATE: 1999-11-25
 PRIOR FILING DATE: 1999-05-11
 NUMBER OF SEQ ID NOS: 26
 SOFTWARE: Patent In Ver. 2.0
 SEQ ID NO 19
 LENGTH: 96
 TYPE: PRT
 ORGANISM: Human immunodeficiency virus type 1
 FEATURE:
 OTHER INFORMATION: vpr protein
 US-09-309-572-19

Query Match 89.0%, Score 461, DB 21, Length 96
 Best Local Similarity 87.5%, Field No 9, 50-49

Matches 84: Conservative 7, Mismatches 5, Indels 0, Gaps 0

QY 1 MEOAEPDGPPEPPYNNWITLLELEKNEAVRPPIWLSIQHITYETGTMVEAL 60
 |||||
 DB 1 MEOAEPDGPPEPPYNNWITLLELEKNEAVRPPIWLSIQHITYETGTMVEAL 60
 QY 61 IRIIQQILFIRIICGHSRIGVIRRRANASRS 96
 |||||
 DB 61 IRIIQQILFIRIICGHSRIGVIRRRANASRS 96

RESULT 7

US-09-422-917A-19

Sequence 19, Application US/09422917A
 GENERAL INFORMATION:
 APPLICANT: Delaporte, Eric
 TITLE OF INVENTION: In Situ Hybridization Probes Pseudotyped with HCMV
 FILE REFERENCE: 950489
 CURRENT APPLICATION NUMBER: US/09-409,572

Query Match 89.0%, Score 461, DB 21, Length 96
 Best Local Similarity 87.5%, Field No 9, 50-49

Matches 84: Conservative 7, Mismatches 5, Indels 0, Gaps 0

QY 1 MEOAEPDGPPEPPYNNWITLLELEKNEAVRPPIWLSIQHITYETGTMVEAL 60
 |||||
 DB 1 MEOAEPDGPPEPPYNNWITLLELEKNEAVRPPIWLSIQHITYETGTMVEAL 60
 QY 61 IRIIQQILFIRIICGHSRIGVIRRRANASRS 96
 |||||
 DB 61 IRIIQQILFIRIICGHSRIGVIRRRANASRS 96

RESULT 7

US-09-422-917A-19

Sequence 19, Application US/09422917A
 GENERAL INFORMATION:
 APPLICANT: Delaporte, Eric
 TITLE OF INVENTION: In Situ Hybridization Probes Pseudotyped with HCMV
 FILE REFERENCE: 950489
 CURRENT APPLICATION NUMBER: US/09-409,572

Query Match	43.8%	Score 227	DB 16	Length 100
Best Local Similarity	51.28	Prod. No. 1e 19		
Matches	12	Mismatches	23	Indels
				0
				Gaps
				0

Search completed: October 3, 2001, 14:23:47
Job time: 160 sec

Keywords: child sexual abuse; disclosure; self-blame; victim blaming

AUTHOR: MONTGOMERY, THOMAS
 TITLE OF INVENTION: HIV Vaccines
 FILING REFERENCE: 1989, 112P
 INVENTION FILING NUMBER: 08/767,249

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1 CORRECT FILING DATE: 1998-07-30
2 PRIOR ATTENTION NUMBER: PCT/EP/98/01191
3 PRIOR FILING DATE: 1996-04-19
4 NUMBER OF CLAIMS: 11
5 SOFTWARE: PatentIn version 4.0
6 SEQ ID NO: 5
7 LENGTH: 78
8 TYPE: FBT
9 ORIGINATOR: Human immunodeficiency virus type 1
10 UNP-007-124-9900-5

```

[illegible]

RESULT 5 RESULT 5
 US-08-101-915-4
 Sequence 4, Application US/08/001915
 Patent No. 5861161
 GENERAL INFORMATION:
 APPLICANT: COHEN, ERIC A.
 APPLICANT: BERGERON, DOMINIQUE
 APPLICANT: CHEIROUNE, FLORENT
 APPLICANT: YAO, XIAO-JIAN
 APPLICANT: FENG, KRISTINE, GARY
 TITLE OF INVENTION: METHOD FOR TREATING HIV HIV VIRUS
 TITLE OF INVENTION: BASED ON HIV 1 VPR REGION PROTEOLYSIS
 NUMBER OF SEQUENCES: 5
 CROSS-REFERENCE: OTHERS
 ADDRESSER: KADNER & JACSON
 STREET: 1001 Avenue 91 place, 101 100-Kensack Avenue
 CITY: KENOSHA
 STATE: N.J.
 COUNTRY: U.S.A.
 ZIP: 07601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS DOS
 SOFTWARE: Patent in Release #1 0, Version #1 25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/001915
 FILING DATE:
 CLASSIFICATION: 536
 ABSTRACT/AGENT INFORMATION:
 NAME: JACKSON, DAVID A.
 REGISTRATION NUMBER: 26,742
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-487-5800
 TELEFAX: 201-344-1684
 TELEX: 134521
 INFORMATION FOR SEQ. 1: NO. 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 72 amino acids
 TYPE: amino acid
 STRATEGIES: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYDROLYTICAL: NO
 US-08-101-915-4

[illegible]

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1 RESULT 6
2 US-08-524-694A-4
3 Sequence 4: Application 05/08/524694A
4 Patent No. 6041081
5
6 GENERAL INFORMATION:
7 APPLICANT: COHEN, ERIC A.
8 APPLICANT: EFFEPPON, Dominique
9 APPLICANT: CHECHKINE, Florent
10 APPLICANT: YAO, Xiao-Jian
11 APPLICANT: PIGNAC-KOBIER, Gary
12 TITLE OF INVENTION: PROTEIN TARGETING INTO HIV VIRIONS BASED
13 TITLE OF INVENTION: ON HIV-1 VPR FUSION MOLECULES
14 NUMBER OF SEQUENCES: 5
15 CORRESPONDENCE ADDRESS:
16 ADDRESSEE: KLAUDER & JACKSON
17 STREET: Georgetown Plaza, 411 Harkness Avenue
18 CITY: Harknessack
19 STATE: N.J.
20 COUNTRY: U.S.A.
21 ZIP: 07601
22
23 COMPUTER READABLE FORM:
24 MEDIUM TYPE: floppy disk
25 COMPUTER: IBM PC compatible
26 OPERATING SYSTEM: PC DOS/MS-DOS
27 SOFTWARE: Patged In Release #1.0, Version #1.25
28 CURRENT APPLICATION DATA:
29 APPLICATION NUMBER: 05/08/524694A
30 FILING DATE: September 7, 1995
31 CLASSIFICATION: 514
32
33 ATTORNEY/AGENT INFORMATION:
34 NAME: JACKSON, David A.
35 REGISTRATION NUMBER: 26,742
36 TELECOMMUNICATION INFORMATION:
37 TELEPHONE: 201-343-5800
38 TELEFAX: 201-343-1684
39 TELEX: 133521
40
41 INFORMATION FOR SEQ. ID NO.: 4:
42 SEQUENCE CHARACTERISTICS:
43 LENGTH: 72 amino acids
44 TYPE: amino acid
45 STRANDEDNESS: single
46 TOPOLOGY: linear
47 MOLECULE TYPE: protein
48 HYPOTHEetical: NO
49
50 US 08 524 694A 4

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	69-78:	Score	61:	DB 3:	Length	72:
	Post-Local Similarity	91.7%	Pred.	1.0e-30:		
Matches	66	Corrected	2	Mismatch	4	Indels
						0
						Gaps
						0:
QY	1	MEANENQNGYPRYINMTELELE	KNAVHRRPR	IMHSGVHYIVGIVGIV	VEVL	60
FL	1	MEATNENQNGYPRYINMTELELE	ELIKNAVHRRPR	IMHSGVHYIVGIVGIV	VEVL	60
QY	61	IRILQQLLITHE	72			
DB	61	IRILQQLLITHE	72			

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100 000000 2 000000 2

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Query Match	41.4%	Score 214.5	DB 2	Length 105
Host Level Similarity	48.9%	Prod. No. 2, to 20		
Matches	47	Conservative 16	Mismatches 24	Indels 7
Gap	2	Exon/Intron	Penalty	60
1	1	1	1	1
2	1	1	1	1
3	1	1	1	1
4	1	1	1	1
5	1	1	1	1
6	1	1	1	1
7	1	1	1	1
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RESULT 10
US-08-659-251-9
: Sequence 9, Application US/08669251
: Patient No. 5883081
: GENERAL INFORMATION:
: APPLICANT: Kraus, Guenter
: APPLICANT: Wang-Staal, Flossie
: APPLICANT: Talbot, Randy
: APPLICANT: Foeschla, Eric
: TITLE OF INVENTION: Isolation of No. 5883081 HIV 2 Proviruses
: NUMBER OF SEQUENCES: 50
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, Eighth Floor
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 in. floppy disk
: SOFTWARE: IBM PC compatible
: OPERATING SYSTEM: MS-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09-485-421
: FILING DATE: No. 5883081 yet assigned
: CLASSIFICATION: C14
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/001,441
: FILING DATE: 26-JUL-1995
: ALIASES/AGENTS INFORMATION:
: NAME: Carrell-Mackowski, Eugenia
: REGISTRATION NUMBER: 37,330
: TELEPHONE: (415) 576-0200
: TELEFAX: (415) 576-0300
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 105 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: FEATURE:
: NAME/KEY: Protein
: LOCATION: 1..105
: OTHER INFORMATION: /note- "vpr protein encoded by HIV 2KR"
US-08-659-251-9

Query Match 36.1% Score 187: DB 2: Length 105:
Best Local Similarity 46.3% Pred. No. 8.1e-17:
Matches 38: Conservative 16: Mismatches 26: Indels 2: Gaps 2:

QY 2 EQAPFQCPQEPYPMWTLLEELKNEVPR-FRLWLSAQHLYTYGDTWVEAL 60
+ + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + +
DB 7 EPPPEDETPRQDEWVGILREIRFELAKHFDRL-LITLQNYICARHCDLTSAREL 65
+ + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + +
QY 61 IRIQQLFIHPRIGGRSRKIG 82
+ + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + +
DB 66 INVADALVIRKACKRSKIG 87
+ + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + +

RESULT 11
US-09-256-490-9
: Sequence 9, Application US/09256490
: Patient No. 6235681
: GENERAL INFORMATION:
: APPLICANT: Kraus, Guenter
: APPLICANT: Wang-Staal, Flossie

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: APPLICANT: Talbot, Randy
: APPLICANT: Foeschla, Eric
: TITLE OF INVENTION: Isolation of No. 6235681 HIV 2 Proviruses
: NUMBER OF SEQUENCES: 50
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, Eighth Floor
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: SOFTWARE: IBM PC compatible
: OPERATING SYSTEM: MS-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09-256-490
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/95-959,251
: FILING DATE:
: ALIASES/AGENTS INFORMATION:
: NAME: Carrell-Mackowski, Eugenia
: REGISTRATION NUMBER: 37,330
: TELEPHONE: (415) 576-0200
: TELEFAX: (415) 576-0300
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 105 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: FEATURE:
: NAME/KEY: Protein
: LOCATION: 1..105
: OTHER INFORMATION: /note- "vpr protein encoded by HIV 2KR"
US-09-256-490-9

Query Match 36.1% Score 187: DB 4: Length 105:
Best Local Similarity 46.3% Pred. No. 8.1e-17:
Matches 38: Conservative 16: Mismatches 26: Indels 2: Gaps 2:

QY 2 EQAPFQCPQEPYPMWTLLEELKNEVPR-FRLWLSAQHLYTYGDTWVEAL 60
+ + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + +
DB 7 EPPPEDETPRQDEWVGILREIRFELAKHFDRL-LITLQNYICARHCDLTSAREL 65
+ + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + +
QY 61 IRIQQLFIHPRIGGRSRKIG 82
+ + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + +
DB 66 INVADALVIRKACKRSKIG 87
+ + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + +

RESULT 12
PCT-US96-11445-9
: Sequence 9, Application PCT/US9611445
: GENERAL INFORMATION:
: APPLICANT: The Regents of the University of California
: TITLE OF INVENTION: Isolation of Novel HIV-2 Proviruses
: NUMBER OF SEQUENCES: 50
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Robbins, Boylmer & Carson
: STREET: 201 N. Figueroa Street, 5th Floor
: CITY: Los Angeles
: STATE: California
: COUNTRY: USA
: ZIP: 90012-2628
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk

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GenCore version 4.5
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us-09-485-421-1

October 3, 2001, 13:40:05, GenCore v4.5, 489,148 Million cell updates/sec

(without alignments)

Perfect score: 518
Sequence: 1 MEGAPROTEOMEPYPMWMT
Database: 1 MEGAPROTEOMEPYPMWMT
Scoring Method: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 20000000

Post-processing: Minimum Match: 0%
Maximum Match: 100%
Listing first 45 Summaries

Database: 1: PIR48*
2: PIR1*
3: PIR2*
4: PIR3*
5: PIR4*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Match	Length	DB	Hit	Description
1	459	88.6	96	2	T09444	vpr protein - huma
2	454	87.6	96	2	S64380	vpr protein - huma
3	448.5	86.6	97	1	E41923	vpr protein - huma
4	445	85.9	96	2	T01670	vpr protein - huma
5	441.5	85.2	95	2	T09343	vpr protein - huma
6	402	77.6	96	1	ASLJSC	vpr protein - simi
7	248	47.9	97	2	S03067	gene R protein - h
8	248	47.9	101	1	ASLJ43	vpr protein - simi
9	247	47.7	89	2	S07391	vpr protein - simi
10	245.5	47.4	101	2	T11564	vpr protein - simi
11	243.5	47.0	122	1	ASLJRS	vpr protein - simi
12	236.5	46.6	105	2	SE0066	vpr protein - huma
13	224	44.8	101	2	S08479	vpr protein - huma
14	221.5	44.2	104	1	ASLJCY	vpr protein - huma
15	214.5	41.4	105	1	ASLJ82	vpr protein - huma
16	210	40.5	104	1	ASLJST	vpr protein - huma
17	207	40.3	105	2	S12156	vpr protein - huma
18	204	39.4	105	1	ASLJ0R	vpr protein - huma
19	193	36.5	104	2	S28083	vpr protein - simi
20	191.5	36.1	140	2	S43361	vpr protein - simi
21	197.5	36.8	119	1	ASLJX4	vpr protein - simi
22	193.5	36.1	112	1	ASLJST	vpr protein - simi
23	192.5	35.7	112	2	SE0066	vpr protein - simi
24	190.5	35.3	112	1	ASLJX3	vpr protein - simi
25	184.5	34.3	112	1	ASLJ0H	vpr protein - huma
26	184.5	34.3	112	2	S07390	vpr protein - simi
27	183.5	34.1	112	2	S12156	vpr protein - huma
28	183	34.0	112	2	T11564	vpr protein - simi
29	176.5	33.3	112	1	ASLJCY	vpr protein - huma

ALIGNMENTS

RESULT 1
T09444
vpr protein - human immunodeficiency virus type 1 (strain JFEL)

C-Species: human immunodeficiency virus type 1, HIV-1
C-Dates: 16-Jul-1999 #sequence_revision 16-Jul-1999 #ext_change 26-Aug-1999

C-Accession: T09444
P-Name: S1; Virens, H.V.; Akashi, T.; O'Brien, W.A.; Chen, L.S.; Koyanagi, Y.; Numaiz
submitted to the EMBL Data Library, July 1996

A-Reference number: Z15673
A-Accession: T09444
A-Species: preliminary; translated from GP/PEL/70DBJ

A-Molecule type: DNA
A-Residues: 1-96 SPAN
A-Cross-references: EMBL:061632; NID:q1465777; PID:q1465784

C-Genetics:
A-Genet: vpr
C-Genet: vpr

Query Match 88.6% Score 459; DB 2; Length 96;

best local similarity 87.5% Prot. No. 2,60-43;
Matches 84; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Q: 1 MEGAPROTEOMEPYPMWMTLELELEKAVVPPVWLSLQHYVYGVWVEAT 60
H: 1 MEGAPROTEOMEPYPMWMTLELELEKAVVPPVWLSLQHYVYGVWVEAT 60

Q: 61 MEGAPROTEOMEPYPMWMTLELELEKAVVPPVWLSLQHYVYGVWVEAT 96
H: 61 MEGAPROTEOMEPYPMWMTLELELEKAVVPPVWLSLQHYVYGVWVEAT 96

RESULT 2
S64380
vpr protein - human immunodeficiency virus type 1

C-Species: human immunodeficiency virus type 1, HIV-1
C-Dates: 15-Jul-1995 #sequence_revision 01-Sep-1995 #ext_change 20-Sep-1999

C-Accession: S64380
P-Name: T1; Buckler White, A.L.
submitted to the EMBL Data Library, July 1989

A-Reference number: S64377
A-Accession: S64380
A-Species: preliminary

A-Molecule type: genomic RNA
A-Residues: 1-96 CDS
A-Cross-references: EMBL:M20779; NID:q1465777; PID:q1465784

C-Genetics: AIDS vpr protein
A-Genet: vpr
C-Genet: vpr

Query Match 87.6% Score 454; DB 2; Length 96;
best local similarity 87.5% Prot. No. 90-43;
Matches 81; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

GenCore version 4.5
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CM protein - protein search, using sw model

Received: 2001, 10:21:47, accepted: 2002, 01:25:22, online: 2002, 02:21:47

493.836 Million cell updates/sec

Title: 55-19-485-42; -1
 Document: 510

Scoring table: **FL0SUM62**

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listed first 45 summaries

Database : SwissProt_49; *

pred. Re. in the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARY

Result	No.	Score	Quesry	Match	Length	DB	LT	Source	Location
1	470	80.7	96	1	VR_HV11R			P05942R human	human
2	464	80.6	96	1	VR_HV11R			P25982R human	human
3	464	80.6	96	1	VR_HV10R			P05936R human	human
4	461	80.6	96	1	VR_HV11R			P15752R human	human
5	459	80.6	96	1	VR_HV11R			P05945R human	human
6	459	80.6	96	1	VR_HV11R			P15751R human	human
7	454	80.6	96	1	VR_HV12R			P15751R human	human
8	452	80.2	96	1	VR_HV11R			P05942R human	human
9	448	80.6	97	1	VR_HV11R			P05942R human	human
10	446	80.1	96	1	VR_HV10R			P25982R human	human
11	445	80.0	97	1	VR_HV1A2			P05945R human	human
12	445	85.9	97	1	VR_HV10R			P05955R human	human
13	402	77.6	96	1	VR_HV11R			P17287R chimpanzee	
14	362	69.9	78	1	VR_HV11R			P05942R human	human
15	358	69.1	78	1	VR_HV1A5			P05942R human	human
16	288	47.9	101	1	VR_HV11R			P05942R human	human
17	217	37.7	89	1	VR_HV1A5			P15752R human	human
18	247	47.7	101	1	VR_HV10R			P15752R human	human
19	246	47.0	97	1	VR_HV10R			P15752R human	human
20	213	47.0	102	1	VR_HV10R			P15752R human	human
21	226	48.7	105	1	VR_HV11R			P15752R human	human
22	226	48.7	105	1	VR_HV12R			P05943R human	human
23	221	48.2	102	1	VR_HV12R			P15752R human	human
24	221	48.2	101	1	VR_HV12R			P15752R human	human
25	211	48.4	105	1	VR_HV12R			P25982R human	human
26	211	40.7	87	1	VR_HV12R			P15752R human	human
27	210	48.6	104	1	VR_HV12R			P15752R human	human
28	207	40.0	105	1	VR_HV12R			P15752R human	human
29	204	39.4	105	1	VR_HV12R			P15752R human	human
30	187	36.1	105	1	VR_HV12R			P15752R human	human
31	159	29.6	101	1	VR_HV12R			P15752R human	human
32	154	21.9	119	1	VR_HV11R			P25982R human	human
33	104	20.9	119	1	VR_HV11R			P25982R human	human

ALIGNMENTS

RESULT	1	STANDARD:	PRT:	96 AA.
1	VRP_HV1BR			
2	VRP_HV1BR			
3	VRP_HV1BR			
4	VRP_HV1BR			
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[illegible]

[illegible]

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01 VR.
02 Human immunodeficiency virus type 1 (MA1 isolate) (HIV-1).
03 Virus33, Recombinant Strains, Recombinant, Lentivirus.
04 NCBI_TaxID=11697;
05
06
07 SEQUENCE FROM N.A.
08 MEDLINE=8415557; PubMed=212612;
09 Alizon M., Main-Hobson S., Montanier L., Sanjo P.:
10 "Genetic variability of the AIDS virus: nucleotide sequence analysis
11 of two isolates from African patients.";
12 Cell 45:63-74(1986).
13
14
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21 or send an email to license@ebi.ac.uk.
22
23 EMBL: X52154; GAA16403.1;
24 P12; S09096; A51J8C.
25 HIV: X52154; VPRSV2.
26
27 Query Match 85.98; Score 445; DB 1; Length 96;
28 First Local Similarity 89.1%; Prod.No. 1.86-41;
29 Matches 92; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
30
31 1 MCAAPRPGGPGPPYNDMTFLLEKKNVNHPPPIWISLQHYVGGTGVFN 60
32
33
34 1 MCAAPRPGGPGPPYNDMTFLLEKKNVNHPPPIWISLQHYVGGTGVFN 60
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37 1 MCAAPRPGGPGPPYNDMTFLLEKKNVNHPPPIWISLQHYVGGTGVFN 60
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95
96
97 1 MCAAPRPGGPGPPYNDMTFLLEKKNVNHPPPIWISLQHYVGGTGVFN 60
98
99
100 1 MCAAPRPGGPGPPYNDMTFLLEKKNVNHPPPIWISLQHYVGGTGVFN 60

```


1

2

10	61	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
10	61	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
10	61	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
10	61	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
10	61	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
10	61	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53</																																															

Query Match:	97.7%	Score 470	E=1e-116	Length 680
Post Local Similarity:	89.6%	Pred. No.	1.5e-45	
Matches	66	Conservative	6	Mismatches 4
				Indels 0
				Gaps 0
CY	1	MEGAPROPHAGEPRESENTATION	PPVAVSVTSWGGT ₁ HTTTGVTATVTC ₆₇	
DB	1	MEGAPROPHAGEPRESENTATION	PELEKNSVRRPRMISLQGHIVETGLMAIVEAL ₆₀	
CY	61	KRLDQLLFTHFRPGHPSFICIGGRSPNASKS ₉₆		
DB	61	KRLDQLLFTHFRPGHPSFICIGGRSKSSKS ₉₆		
RESULT 14				
CYE247				
ID	Q9E247	PRELIMINARY:	PTI:	96 AA.
AC	Q9E247:			
D	01-MAR-2001	(TrEMBL)	16	(Created)
F	01-MAR-2001	(TrEMBL)	16	(Last sequence update)
J	01-MAR-2001	(TrEMBL)	16	(Last annotation update)
DE	VIR PROTEIN (TRACHELY).			
GN	VPR.			
OS	Human immunodeficiency virus type 1.			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.			
OX	NCH_1taxid=11676;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN MT4.3;			
RA	Almud N.; Vedrali J.; V.S.R.K.;			
R1	"Low Conservation of Functional Domains of Human Immunodeficiency Virus Type 1 VII and vpr Genes Correlates with Lack of Vertical Transmission.";			
RT	Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.			
DR	EMBL: AF275129; AAC22278.1; -			
FC	N.N.IER	96		
SQ	SEQUENCE	96 AA:	1148 MW:	0660PSC875196810 CRCSd:

[illegible]

QY	61	TRIGQITFHFRIGFRIGFICIGQDFRPNASKS	96
DB	61	KRIIGQITFHFRIGFRIGFICIGQDFRPNASKS	96
RESULT	15		
Q9E246			
16	Q9E246	PROLIMINARY	96 AA
AC	Q9E246		
DE	01 MAR-2001 (1)EMBL:1, 16, (Created)		
DT	01 MAR-2001 (1)EMBL:1, 16, (Last sequence update)		
DI	01 MAR-2001 (1)EMBL:1, 16, (Last annotation update)		
DR	VIR PROTEIN (VIRACIN)		
GN	VIR		
OS	Human immunodeficiency virus type 1		
OC	Virus; Retrovirus; Retroviridae; Lentivirinae		
OX	NTL_TAXID:11676;		
RI	111		
RP	GENBANK F036785.1		
SC	GENBANK F036785.1		
RA	Almad N, Yoshitani V, K.R.		
RT	"Low Efficiency of Functional Isolation of Human Immunodeficiency Virus Type 1 and HTLV-1 Virus by Serial Dilution."		
PL	Journal of Virology		
PM	1991; 65(12):2279-81		
PP	96		
SD	SHOULD: 96 AA, 11588 MB; 069DF0C875196810 CRC32:		

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Query Match: 90.78; Score 470; DB 14; Length 96;
Match Position: 65-93; First Met. 1-45;
Matches: 86; Conservative: 6; Mismatches: 4; Indels: 0; Gaps: 0;

QY 1 MEQAFEDQAGKRYPMWLTLEFEKNEAHPRIWISLQHYVYQHTVEAL 50
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1 MEQAFEDQAGKRYPMWLTLEFEKNEAHPRIWISLQHYVYQHTVEAL 60

QY 61 IRIIQQLLETHFRIGFRASPGIQQPPTKNDASKS 96
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 61 IRIIQQLLETHFRIGFRASPGIQQPPTKNDASKS 96

Search completed: October 7, 2001, 11:24:26
Job time: 184 sec

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Wed Oct 3 13:40:06 2001

us-09-485-421-1.rspt

Page 6

Example: HIV-1 gp120 Enriched.

XX The present invention describes a conjugate composition comprising a
XX treatment of HIV-1 or non HIV-1 Vpr protein conjugated to a therapeutic
XX compound. The conjugate can be used in a method for inhibiting cell
XX proliferation. It can also be used for treating an individual who has a
XX hyperproliferative disease. The HIV-1 Vpr or non HIV-1 Vpr protein
XX treatment can be used for identifying compounds that inhibit Vpr protein
XX binding to the p6 domain of p55 or to p6 protein. The present sequence
XX represents a HIV protein sequence.

XX Sequence: 96 AA.

Query Match: 100.0%; Score: 20; Pos: Length: 96
Best Local Similarity: 100.0%; Pos: 276-12;
Matches: 276 conservative 0; Mismatches: 0; Gaps: 0;
1 TWTEELTEELKNEAVKPPR 20
11111111111111111111
17 dwfclloekknowdrpp 96

RESULT: 2

AAW99812

10 AAW99812 standard: protein: 96 AA.

XX AAW99812

XX 08 JUN 1999 (first entry)

XX HIV Vpr protein sequence #1.

XX HIV Vpr: human immunodeficiency virus; hyperproliferative disease;
XX cell proliferation.

XX Human immunodeficiency virus.

XX W090412-A1.

XX 25 FEB 1999.

XX 14 AUG 1997 98W01081800.

XX 14 AUG 1997 970810056754.

XX (GPRF) HIV-1 HENNYVANIA.

XX AAY9999 V. Kibret Emmanu E. Michaelian S. Patel M.

XX Weiner 199.

XX W01: 1999 101154/15.

XX Conjugate composition comprising HIV-1 Vpr protein treatment - used
XX to inhibit cell proliferation, and treating hyperproliferative
XX disease.

XX Example: HIV-1 gp120 Enriched.

XX The present invention describes a conjugate composition comprising a
XX treatment of HIV-1 or non HIV-1 Vpr protein conjugated to a therapeutic
XX compound. The conjugate can be used in a method for inhibiting cell
XX proliferation. It can also be used for treating an individual who has a
XX hyperproliferative disease. The HIV-1 Vpr or non HIV-1 Vpr protein
XX treatment can be used for identifying compounds that inhibit Vpr protein
XX binding to the p6 domain of p55 or to p6 protein. The present sequence
XX represents a HIV protein sequence.

XX Sequence: 96 AA.

Query Match: 100.0%; Score: 20; Pos: Length: 96
Best Local Similarity: 100.0%; Pos: 276-12;

Matches: 20; conservative 0; Mismatches: 0; Gaps: 0;

07 1 TWTEELTEELKNEAVKPPR 20
11111111111111111111
08 17 dwfclloekknowdrpp 96

RESULT: 4

AAW99812

10 AAW99812 standard: protein: 96 AA.

XX AAW99812

XX 08 JUN 1999 (first entry)

XX HIV-1 Vpr protein.

XX HIV Vpr: human immunodeficiency virus; hyperproliferative disease;
XX cell proliferation.

XX Human immunodeficiency virus type 1.

XX W090412-A1.

XX 25 FEB 1999.

XX 14 AUG 1997 98W01081800.

XX 14 AUG 1997 970810056754.

XX (GPRF) HIV-1 HENNYVANIA.

XX AAY9999 V. Kibret Emmanu E. Michaelian S. Patel M.

XX Weiner 199.

XX W01: 1999 101154/15.

XX Conjugate composition comprising HIV-1 Vpr protein treatment - used
XX to inhibit cell proliferation, and treating hyperproliferative
XX disease.

XX Example: HIV-1 gp120 Enriched.

XX The present invention describes a conjugate composition comprising a
XX treatment of HIV-1 or non HIV-1 Vpr protein conjugated to a therapeutic
XX compound. The conjugate can be used in a method for inhibiting cell
XX proliferation. It can also be used for treating an individual who has a
XX hyperproliferative disease. The HIV-1 Vpr or non HIV-1 Vpr protein
XX treatment can be used for identifying compounds that inhibit Vpr protein
XX binding to the p6 domain of p55 or to p6 protein. The present sequence
XX represents a HIV-1 Vpr protein sequence.

XX Sequence: 96 AA.

Query Match: 100.0%; Score: 20; Pos: Length: 96
Best Local Similarity: 100.0%; Pos: 276-12;

Matches: 20; conservative 0; Mismatches: 0; Gaps: 0;
07 1 TWTEELTEELKNEAVKPPR 20
11111111111111111111
08 17 dwfclloekknowdrpp 96

RESULT: 4

AAW99815

10 AAW99815 standard: protein: 96 AA.

XX AAW99815

XX 08 JUN 1999 (first entry)

XX HIV Vpr wt protein sequence.


```

XX HIV: Virus: Immunodeficiency virus; hyperproliferative disease;
KM cell proliferation.
KM Human immunodeficiency virus.
XX W: 990412-AL.
XX 25-FEB-1999.
XX 14-AUG-1998; 98WO-0516890.
XX 14-AUG-1997; 97US-0055754.
XX (DDBP-) HIV HENRYSLAVIA.
XX Ayyappa V, Kishor-Premnas T, Mahalingam S, Patel M.
XX Weiner DB;
XX WPI: 1999-181154/15.
XX Conjugate composition comprising HIV-1 Vpr protein fragment - used
XX to inhibit cell proliferation, and treating hyperproliferative
XX diseases
XX Example: Fig 1b; 64pp; English.
XX The present invention describes a conjugate composition comprising a
XX fragment of HIV-1 or non-HIV-1 Vpr protein conjugated to a therapeutic
XX compound. The conjugate can be used in a method for inhibiting cell
XX proliferation. It can also be used for treating an individual who has a
XX hyperproliferative disease. The HIV-1 Vpr or non-HIV-1 Vpr protein
XX fragments can be used for identifying compounds that inhibit Vpr protein
XX binding to the p6 domain of p55 or to p6 protein. The present sequence
XX represents an HIV protein sequence.
XX Sequence 96 AA:
XX
XX Query Match 100.0%; Score 20; 14 20; Length 96;
XX Best Local Similarity 100.0%; Pred. No. 2,7c-12;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 DWTLELLPEKKNVAVRPPR 20
XX (|||||)
XX 17 dwtllellpekknavrppr 46
XX
XX RESULT 5
XX AAW99821
XX AAW99821 standard; protein; 96 AA.
XX AA
XX AAW99820;
XX 08-JUN-1999 (first entry)
XX HIV ASyE protein sequence.
XX HIV ASyE protein sequence.
XX HIV: Vpr; human immunodeficiency virus; hyperproliferative disease;
XX cell proliferation.
XX Human immunodeficiency virus
XX W: 990412-AL.
XX 25-FEB-1999.
XX 14-AUG-1998; 98WO-0516890.
XX 14-AUG-1997; 97US-0055754.
XX (DDBP-) HIV HENRYSLAVIA.

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PI Ayyappa V, Kishor-Premnas T, Mahalingam S, Patel M.
PI Weiner DB;
PI WPI: 1999-181154/15.
PI Conjugate composition comprising HIV-1 Vpr protein fragment - used
PI to inhibit cell proliferation, and treating hyperproliferative
PI diseases
PI Example: Fig 1b; 64pp; English.
PI The present invention describes a conjugate composition comprising a
PI fragment of HIV-1 or non-HIV-1 Vpr protein conjugated to a therapeutic
PI compound. The conjugate can be used in a method for inhibiting cell
PI proliferation. It can also be used for treating an individual who has a
PI hyperproliferative disease. The HIV-1 Vpr or non-HIV-1 Vpr protein
PI fragments can be used for identifying compounds that inhibit Vpr protein
PI binding to the p6 domain of p55 or to p6 protein. The present sequence
PI represents an HIV protein sequence.
PI Sequence 96 AA:
PI
PI Query Match 100.0%; Score 20; 14 20; Length 96;
PI Best Local Similarity 100.0%; Pred. No. 2,7c-12;
PI Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
PI
PI 1 DWTLELLPEKKNVAVRPPR 20
PI (|||||)
PI 17 dwtllellpekknavrppr 46
PI
PI RESULT 6
PI AAW99821
PI AAW99821 standard; protein; 96 AA.
PI AA
PI AAW99821;
PI 08-JUN-1999 (first entry)
PI HIV L64S protein sequence.
PI HIV L64S protein sequence.
PI HIV: Vpr; human immunodeficiency virus; hyperproliferative disease;
PI cell proliferation.
PI Human immunodeficiency virus.
PI W: 990412-AL.
PI 25-FEB-1999.
PI 14-AUG-1998; 98WO-0516890.
PI 14-AUG-1997; 97US-0055754.
PI (DDBP-) HIV HENRYSLAVIA.
PI Ayyappa V, Kishor-Premnas T, Mahalingam S, Patel M.
PI Weiner DB;
PI WPI: 1999-181154/15.
PI Conjugate composition comprising HIV-1 Vpr protein fragment - used
PI to inhibit cell proliferation, and treating hyperproliferative
PI diseases
PI Example: Fig 1b; 64pp; English.
PI The present invention describes a conjugate composition comprising a
PI fragment of HIV-1 or non-HIV-1 Vpr protein conjugated to a therapeutic
PI compound. The conjugate can be used in a method for inhibiting cell
PI proliferation. It can also be used for treating an individual who has a
PI hyperproliferative disease. The HIV-1 Vpr or non-HIV-1 Vpr protein

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XX 25-FEB-1999
XX 14-AUG-1998; 98W0-0S16890.
XX 14-AUG-1997; 97US-0055754.
XX (TYPE ) ONIV PENNSYLVANIA.
XX Agyvvo V. Kieber-Emmens T. Mahalingam S. Patel M.
XX Weiner DB;
XX WP1: 1999-181154/15.
XX Conjugate composition comprising HIV-1 Vpr protein fragment - used
XX to inhibit cell proliferation, and treating hyperproliferative
XX diseases
XX Example: Fig 1B; 64pp; English.
XX
XX The present invention describes a conjugate composition comprising a
XX fragment of HIV-1 or non-HIV-1 Vpr protein conjugated to a therapeutic
XX compound. The conjugate can be used in a method for inhibiting cell
XX proliferation. It can also be used for treating an individual who has a
XX hyperproliferative disease. The HIV-1 Vpr or non-HIV-1 Vpr protein
XX fragments can be used for identifying compounds that inhibit Vpr protein
XX binding to the p6 domain of p55 or to p6 protein. The present sequence
XX represents an HIV protein sequence.
XX
XX Sequence 96 AA:
XX
XX Query Match 100.0%; Score 20; DB 20; Length 96;
XX Best Local Similarity 100.0%; Pred. No. 2,76-12;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TWTHLLELLENAVERHPR 20
XX |||||
XX 17 dwtclleclknvvrhpr 46
XX
XX RESULT 10
XX AAW9825
XX 14-AUG-1998; 98W0-0S16890.
XX AAW9825.
XX 08-JUN-1999 (first entry)
XX HIV H71V protein sequence.
XX HIV Vpr; human immunodeficiency virus; hyperproliferative disease;
XX cell proliferation.
XX Human immunodeficiency virus.
XX W0990412-A1.
XX 25-FEB-1999.
XX 14-AUG-1998; 98W0-0S16890.
XX 14-AUG-1997; 97US-0055754.
XX (TYPE ) ONIV PENNSYLVANIA.
XX Agyvvo V. Kieber-Emmens T. Mahalingam S. Patel M.
XX Weiner DB;
XX WP1: 1999-181154/15.
XX Conjugate composition comprising HIV-1 Vpr protein fragment - used
XX to inhibit cell proliferation, and treating hyperproliferative

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PT diseases
XX Example: Fig 1B; 64pp; English.
XX
XX The present invention describes a conjugate composition comprising a
XX fragment of HIV-1 or non-HIV-1 Vpr protein conjugated to a therapeutic
XX compound. The conjugate can be used in a method for inhibiting cell
XX proliferation. It can also be used for treating an individual who has a
XX hyperproliferative disease. The HIV-1 Vpr or non-HIV-1 Vpr protein
XX fragments can be used for identifying compounds that inhibit Vpr protein
XX binding to the p6 domain of p55 or to p6 protein. The present sequence
XX represents an HIV protein sequence.
XX
XX Sequence 96 AA:
XX
XX Query Match 100.0%; Score 20; DB 20; Length 96;
XX Best Local Similarity 100.0%; Pred. No. 2,76-12;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TWTHLLELLENAVERHPR 20
XX |||||
XX 17 dwtclleclknvvrhpr 36
XX
XX RESULT 11
XX AAW9826
XX 14-AUG-1998; 98W0-0S16890.
XX AAW9826.
XX 08-JUN-1999 (first entry)
XX HIV G75A protein sequence.
XX HIV Vpr; human immunodeficiency virus; hyperproliferative disease;
XX cell proliferation.
XX Human immunodeficiency virus.
XX W0990412 A1.
XX 25-FEB-1999.
XX 14-AUG-1998; 98W0-0S16890.
XX 14-AUG-1997; 97US 0055754.
XX (TYPE ) ONIV PENNSYLVANIA.
XX Agyvvo V. Kieber-Emmens T. Mahalingam S. Patel M.
XX Weiner DB;
XX WP1: 1999-181154/15.
XX Conjugate composition comprising HIV 1 Vpr protein fragment - used
XX to inhibit cell proliferation, and treating hyperproliferative
XX diseases
XX Example: Fig 1B; 64pp; English.
XX
XX The present invention describes a conjugate composition comprising a
XX fragment of HIV-1 or non-HIV-1 Vpr protein conjugated to a therapeutic
XX compound. The conjugate can be used in a method for inhibiting cell
XX proliferation. It can also be used for treating an individual who has a
XX hyperproliferative disease. The HIV-1 Vpr or non-HIV-1 Vpr protein
XX fragments can be used for identifying compounds that inhibit Vpr protein
XX binding to the p6 domain of p55 or to p6 protein. The present sequence
XX represents an HIV protein sequence.
XX
XX Sequence 96 AA:

```


WP1: 2960-27043723

XX Expression vector useful for reducing infectivity of HIV or for
PI targeting into HIV viruses, comprises nucleic acid segment encoding
PI recombinant or chimeric protein consisting of a Vpr/Vpr2 fusion
PI incorporation domain.

PS Claim 1: (vaccine 9-10) 37pp; English.

XX The present invention describes an expression vector (1) comprising a
CC nucleic acid segment encoding a recombinant protein for interfering with
CC the incorporation of native Vpr/Vpr2 into HIV-1 or HIV-2 virion or a
CC chimeric protein that is incorporated into an HIV-1 or HIV-2 virion,
CC operably linked to a promoter. Also described are: (1) an expression
CC eukaryotic or prokaryotic cell transformed with (1); (2) a composition
CC for reducing infectivity of HIV-1 or HIV-2 in vitro comprising an
CC effective amount of (1) in association with a pharmaceutically
CC acceptable carrier; and (3) a composition for targeting into an HIV-1 or
CC HIV-2 virion comprising an effective amount of (1) in association with a
CC pharmaceutically acceptable carrier. (1) has anti-HIV activity and can
CC be used in gene therapy. (1) is useful for reducing infectivity of HIV
CC in vitro and for targeting into HIV-1 or HIV-2 virion. The present
CC sequence represents the Vpr protein from HIV, which is used in the
CC exemplification of the present invention.

SQ Sequence 72 AA:

Query Match 95.0%; Score 19; DB 21; Length 72;

Host Local Similarity 100.0%; Ident. No. 1,86-11;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

07 2 WLELEELKNEAVRHPK 20

|||||111111111111

1b 18 WLELEELKNEAVRHPK 36

RESULT 15

AAB69307

1D AAB69307 standard; Protein; 95 AA.

XX AAB69307:

DT 20-APR-2001 (first entry)

EE HIV-1 non-subtype B clone 94CY032-3 Vpr protein.

XX HIV-1: human immunodeficiency virus; non-subtype B; gag; pol; env;

FW vpr; vif; tat; rev; nef; vaccine.

XX Human immunodeficiency virus type 1.

FN W02/0026416-A1.

XX 11-MAY-2001.

PE 25-OCT-1999; 99WO-0824837.

XX 02-NOV-1998; 98US-0184418.

PA (0A88-) GAG RES. FOUND.

PI Hahn BH, Shaw GM, Gao F;

XX WP1: 2960-065651/31.

XX Novel genomic nucleic acids of non-subtype B human immunodeficiency

PI virus type 1 useful for detecting and treating AIDS comprises a

PI specific nucleotide sequence.

PS Claim 41: Fig 17: 14pp; English.

XX The present invention provides the protein and coding sequences for a

CC nucleic acid segment encoding a recombinant protein for interfering with
CC the incorporation of native Vpr/Vpr2 into HIV-1 or HIV-2 virion or a
CC chimeric protein that is incorporated into an HIV-1 or HIV-2 virion,
CC operably linked to a promoter. Also described are: (1) an expression
CC eukaryotic or prokaryotic cell transformed with (1); (2) a composition
CC for reducing infectivity of HIV-1 or HIV-2 in vitro comprising an
CC effective amount of (1) in association with a pharmaceutically
CC acceptable carrier; and (3) a composition for targeting into an HIV-1 or
CC HIV-2 virion comprising an effective amount of (1) in association with a
CC pharmaceutically acceptable carrier. (1) has anti-HIV activity and can
CC be used in gene therapy. (1) is useful for reducing infectivity of HIV
CC in vitro and for targeting into HIV-1 or HIV-2 virion. The present
CC sequence represents the Vpr protein from HIV, which is used in the
CC exemplification of the present invention.

SQ Sequence 95 AA:

Query Match 95.0%; Score 19; DB 21; Length 95;

Host Local Similarity 100.0%; Ident. No. 2,46-11;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

07 2 WLELEELKNEAVRHPK 20

|||||111111111111

1b 18 WLELEELKNEAVRHPK 36

Search completed: 09/06/01 3, 2001, 13:25:20

Job time: 188 sec

GenCore Version 4.5
Copyright (c) 1997 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 3, 2001, 13:23:42, Search time 18.81 Seconds
(without alignments)
21,893 Million cell updates/sec

Title: US-09-485-421-1_COPY_17_36

26

Sequence: 1 DMTLELEIKHEVNIHFR 20

Scoring table:

Gapop 60.0, Gapext 60.0

Searched: 197339 seqs, 20590346 residues

Word size: 0

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 290000000

Post processing: listing first 45 summaries

Database: Issued_Patents_AA *

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2: /home/bj/fredrickson/seq/seq_5B_G0M3.pat.*
3: /home/bj/fredrickson/seq/seq_5A_G0M3.pat.*
4: /home/bj/fredrickson/seq/seq_5B_G0M3.pat.*
5: /home/bj/fredrickson/seq/seq_5A_G0M3.pat.*
6: /home/bj/fredrickson/seq/seq_5B_G0M3.pat.*

Print. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
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2	19	95.0	72 3 US-08-301-915-4	Sequence 4, App1
3	19	95.0	78 4 US-09-124-900-5	Sequence 5, App1
4	19	95.0	46 7 US-08-101-915-1	Sequence 1, App1
5	19	95.0	96 3 US-08-524-694A-1	Sequence 15, App1
6	10	50.0	96 3 US-08-704-8560-15	Sequence 15, App1
7	8	40.0	18 3 US-08-940-095-196	Sequence 196, App
8	8	40.0	18 3 US-08-940-095-196	Sequence 196, App
9	9	40.0	18 3 US-08-940-095-196	Sequence 196, App
10	7	35.0	16 3 US-08-940-095-253	Sequence 253, App
11	7	35.0	16 3 US-08-940-093-253	Sequence 253, App
12	7	35.0	16 3 US-08-940-096-253	Sequence 253, App
13	7	35.0	19 3 US-08-940-095-191	Sequence 191, App
14	7	35.0	18 3 US-08-940-095-192	Sequence 192, App
15	7	35.0	18 3 US-08-940-095-194	Sequence 193, App
16	7	35.0	18 3 US-08-940-095-194	Sequence 194, App
17	7	35.0	18 3 US-08-940-095-195	Sequence 195, App
18	7	35.0	18 3 US-08-940-095-197	Sequence 197, App
19	7	35.0	18 3 US-08-940-095-198	Sequence 198, App
20	7	35.0	18 3 US-08-940-095-200	Sequence 200, App
21	7	35.0	18 3 US-08-940-095-201	Sequence 201, App
22	7	35.0	18 3 US-08-940-095-203	Sequence 203, App
23	7	35.0	18 3 US-08-940-095-204	Sequence 204, App
24	7	35.0	18 3 US-08-940-095-206	Sequence 206, App
25	7	35.0	18 3 US-08-940-095-207	Sequence 207, App
26	7	35.0	18 3 US-08-940-095-210	Sequence 210, App
27	7	35.0	18 3 US-08-940-095-214	Sequence 214, App

ALIGNMENTS

28	7	35.0	18 3 US-08-940-095-216	Sequence 216, App
29	7	35.0	18 3 US-08-940-095-221	Sequence 221, App
30	7	35.0	18 3 US-08-940-095-231	Sequence 231, App
31	7	35.0	18 3 US-08-940-093-191	Sequence 191, App
32	7	35.0	18 3 US-08-940-093-192	Sequence 192, App
33	7	35.0	18 3 US-08-940-093-193	Sequence 193, App
34	7	35.0	18 3 US-08-940-093-194	Sequence 194, App
35	7	35.0	18 3 US-08-940-093-195	Sequence 195, App
36	7	35.0	18 3 US-08-940-093-197	Sequence 197, App
37	7	35.0	18 3 US-08-940-093-198	Sequence 198, App
38	7	35.0	18 3 US-08-940-093-200	Sequence 200, App
39	7	35.0	18 3 US-08-940-093-201	Sequence 201, App
40	7	35.0	18 3 US-08-940-093-203	Sequence 203, App
41	7	35.0	18 3 US-08-940-093-204	Sequence 204, App
42	7	35.0	18 3 US-08-940-093-206	Sequence 206, App
43	7	35.0	18 3 US-08-940-093-207	Sequence 207, App
44	7	35.0	18 3 US-08-940-093-210	Sequence 210, App
45	7	35.0	18 3 US-08-940-093-214	Sequence 214, App

RESULT 1

US-08-301-915-4

Sequence 4, Application US/08301915

Patent No. 5861161

GENERAL INFORMATION:

APPLICANT: COHEN, ERIC A.

APPLICANT: BERKSON, Dominique

APPLICANT: CHEPPOINE, Florent

APPLICANT: YAO, Xiao-Lian

APPLICANT: FICHAS, Christophe, Gary

TITLE OF INVENTION: PROTEIN INHIBITING HIV VIRIONS

INVENTOR: N. RASER OR HIV-1 VIF PROTEIN MOLECULES

INVENTOR: N. RASER OR HIV-1 VIF PROTEIN MOLECULES

INVENTOR: N. RASER OR HIV-1 VIF PROTEIN MOLECULES

INVENTOR: N. RASER OR HIV-1 VIF PROTEIN MOLECULES

INVENTOR: N. RASER OR HIV-1 VIF PROTEIN MOLECULES

INVENTOR: N. RASER OR HIV-1 VIF PROTEIN MOLECULES

INVENTOR: N. RASER OR HIV-1 VIF PROTEIN MOLECULES

INVENTOR: N. RASER OR HIV-1 VIF PROTEIN MOLECULES

INVENTOR: N. RASER OR HIV-1 VIF PROTEIN MOLECULES

INVENTOR: N. RASER OR HIV-1 VIF PROTEIN MOLECULES

INVENTOR: N. RASER OR HIV-1 VIF PROTEIN MOLECULES

INVENTOR: N. RASER OR HIV-1 VIF PROTEIN MOLECULES

INVENTOR: N. RASER OR HIV-1 VIF PROTEIN MOLECULES

INVENTOR: N. RASER OR HIV-1 VIF PROTEIN MOLECULES

INVENTOR: N. RASER OR HIV-1 VIF PROTEIN MOLECULES

INVENTOR: N. RASER OR HIV-1 VIF PROTEIN MOLECULES

INVENTOR: N. RASER OR HIV-1 VIF PROTEIN MOLECULES

INVENTOR: N. RASER OR HIV-1 VIF PROTEIN MOLECULES

INVENTOR: N. RASER OR HIV-1 VIF PROTEIN MOLECULES

INVENTOR: N. RASER OR HIV-1 VIF PROTEIN MOLECULES

INVENTOR: N. RASER OR HIV-1 VIF PROTEIN MOLECULES

INVENTOR: N. RASER OR HIV-1 VIF PROTEIN MOLECULES

INVENTOR: N. RASER OR HIV-1 VIF PROTEIN MOLECULES

INVENTOR: N. RASER OR HIV-1 VIF PROTEIN MOLECULES

INVENTOR: N. RASER OR HIV-1 VIF PROTEIN MOLECULES

INVENTOR: N. RASER OR HIV-1 VIF PROTEIN MOLECULES

INVENTOR: N. RASER OR HIV-1 VIF PROTEIN MOLECULES

INVENTOR: N. RASER OR HIV-1 VIF PROTEIN MOLECULES

INVENTOR: N. RASER OR HIV-1 VIF PROTEIN MOLECULES

INVENTOR: N. RASER OR HIV-1 VIF PROTEIN MOLECULES

INVENTOR: N. RASER OR HIV-1 VIF PROTEIN MOLECULES

INVENTOR: N. RASER OR HIV-1 VIF PROTEIN MOLECULES

INVENTOR: N. RASER OR HIV-1 VIF PROTEIN MOLECULES

INVENTOR: N. RASER OR HIV-1 VIF PROTEIN MOLECULES

INVENTOR: N. RASER OR HIV-1 VIF PROTEIN MOLECULES

INVENTOR: N. RASER OR HIV-1 VIF PROTEIN MOLECULES

INVENTOR: N. RASER OR HIV-1 VIF PROTEIN MOLECULES

US-08-401-915-1

Query Match 95.0%; Score 19; DB 2; Length 96;
 Best Local Similarity 100.0%; Prod. No. 2-5c-11;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

07 2 WTELELEKNAVHEHT 20
 18 WTELELEKNAVHEHT 16

RESULT 5
 US-08-524-694A-1

Sequence 1, Application US/08524694A
 Patent No. 6043081
 GENERAL INFORMATION:
 APPLICANT: COHEN, ERIC A.
 APPLICANT: BECKER, Florence
 APPLICANT: CHESTNUT, Florence
 APPLICANT: VA, CDC, JPL
 APPLICANT: FICHAG KOSMIR, Gary
 TITLE OF INVENTION: PROTEIN TARGETING INTO HIV VIRIONS BASED
 TITLE OF INVENTION: ON HIV-1 VPR FUSION MOLECULES
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: KLAUSER & JACKSON
 STREET: Continental Plaza, 411 Hackensack Avenue
 CITY: Hackensack
 STATE: N.J.
 COUNTRY: U.S.A.
 ZIP: 07601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/098/524,694A
 FILING DATE: September 7, 1995
 CLASSIFICATION: 514
 ATTORNEY/AGENT: NESTEMATTIN
 NAME: JACKSON, David A.
 REGISTRATION NUMBER: 26,742
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-487-5809
 TELEFAX: 201-443-1684
 TELETYPE: 145521
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 96 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 Molecule type: protein
 HYDROTHERICAL: NO
 US-08-524-694A-1

Query Match 95.0%; Score 19; DB 4; Length 96;
 Best Local Similarity 100.0%; Prod. No. 2-5c-11;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

07 2 WTELELEKNAVHEHT 20
 18 WTELELEKNAVHEHT 16

RESULT 6
 US-08-704-856C-15
 Sequence 15, Application US/08704856C
 Patent No. 6042842
 GENERAL INFORMATION:

APPLICANT: Kufrowski, Hilary
 APPLICANT: Yusibov, Vidadi
 APPLICANT: Hooper, Douglas, C.
 APPLICANT: Modelska, Anna
 TITLE OF INVENTION: Polypeptides fused with Plant Virus
 TITLE OF INVENTION: Coal Proteins
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Allan H. Fiedel & Associates
 STREET: 1525 Locust Street, 15th floor
 CITY: Philadelphia
 STATE: Pennsylvania
 COUNTRY: USA
 ZIP: 19102

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: MS DOS
 SOFTWARE: Corel WordPerfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/098/704,856C
 FILING DATE: 28-Aug-1996
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Fiedel, Allan H.
 REGISTRATION NUMBER: 41,253
 REFERENCE/INCKET NUMBER: 119-097
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 732-7090
 TELEFAX: (215) 732-7090
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 96 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 HYDROTHERICAL: N
 US-08-704-856C-15

Query Match 50.0%; Score 10; DB 3; Length 96;
 Best Local Similarity 100.0%; Prod. No. 0.0057;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

07 2 WTELELEK 11
 18 WTELELEK 27

RESULT 7
 US-08-940-095-196

Sequence 196, Application US/08940095
 Patent No. 6004925
 GENERAL INFORMATION:
 APPLICANT: Hussaux, Jean-Louis
 APPLICANT: Sekul, Renate
 APPLICANT: Buttner, Klaus
 APPLICANT: Cornut, Isabelle
 APPLICANT: Metz, Gunther
 APPLICANT: Infourty, Jean
 TITLE OF INVENTION: ANTIFERRETIN A-1 AGONISTS
 TITLE OF INVENTION: AND THEIR USE TO TREAT ENCEPHALOPATHIC DISORDERS
 NUMBER OF SEQUENCES: 298
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Imvite & Edwards LLP
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10036-2011
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM compatible
 OPERATING SYSTEM: DOS

```

1  SOFTWARE: FASTSEQ Version 2.00
2  CURRENT APPLICATION DATA:
3  FILING DATE: 29 SEP 1997
4  CLASSIFICATION: 911
5  PRIOR APPLICATION DATA:
6  APPLICATION NUMBER:
7  FILING DATE:
8  ATTORNEY/AGENT INFORMATION:
9  NAME: CORUZZI, Laura A
10 REGISTRATION NUMBER: 40,742
11 REFERENCE/KEY NUMBER: 009196-0006 999
12 TELECOMMUNICATION INFORMATION:
13 TELEPHONE: 650-493-4945
14 TELEFAX: 650-493-5556
15 TELETEXT: 66141 PENNIE
16 INFORMATION FOR SEQ ID NO: 196:
17 SEQUENCE CHARACTERISTICS:
18 LENGTH: 18 amino acids
19 TYPE: amino acid
20 STANDARDS: single
21 MOLECULE TYPE: No. 604742e
22 FEATURES:
23 NAME/KEY: other
24 LOCATION: 1-18
25 OTHER INFORMATION: N terminal acetylated and
26 OTHER INFORMATION: C terminal unaltered
27 US-09-485-421-196

```

```

Query Match 40.0% Score 87 108 42 Length 182
Post Local Similarity 100.0% Prod. No. 0.12
Matches 82 Conservative 02 Mismatches 02 Indels 02 Gaps 02
5 ELITEKIN 12
1111111
10 8 ELITEKIN 15

```

```

1  RESULT 8
2  US-09-485-421-196
3  Sequence 196, Application US/09/040996
4  Patent No. 604742
5  GENERAL INFORMATION:
6  APPLICANT: Bassoux, Jean Louis
7  APPLICANT: Sokol, Renato
8  APPLICANT: Butnot, Klaus
9  APPLICANT: Coruza, Isabelle
10 APPLICANT: Molz, Gunter
11 TITLE OF INVENTION: APO-LIPROTEIN A-1 AGONISTS
12 NUMBER OF SEQUENCES: 254
13 CORRESPONDENCE ADDRESS:
14 ADDRESSEE: Bonito & Edwards LLP
15 STREET: 1155 Avenue of the Americas
16 CITY: New York
17 STATE: NY
18 COUNTRY: USA
19 ZIP: 10046-2811
20 COMPUTER READABLE FORM:
21 MEDIUM TYPE: Diskette
22 COMPUTER: IBM Compat 486
23 OPERATING SYSTEM: DOS
24 SOFTWARE: FASTSEQ Version 2.00
25 CURRENT APPLICATION DATA:
26 FILING DATE: 29 SEP 1997
27 CLASSIFICATION: 911
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER:
30 FILING DATE:
31 ATTORNEY/AGENT INFORMATION:

```

```

1  NAME: CORUZZI, Laura A
2  REGISTRATION NUMBER: 40,742
3  REFERENCE/KEY NUMBER: 009196-0006 999
4  TELECOMMUNICATION INFORMATION:
5  TELEPHONE: 650-493-4945
6  TELEFAX: 650-493-5556
7  TELETEXT: 66141 PENNIE
8  INFORMATION FOR SEQ ID NO: 196:
9  SEQUENCE CHARACTERISTICS:
10 LENGTH: 18 amino acids
11 TYPE: amino acid
12 STANDARDS: single
13 MOLECULE TYPE: No. 604742e
14 FEATURES:
15 NAME/KEY: other
16 LOCATION: 1-18
17 OTHER INFORMATION: N terminal acetylated and
18 OTHER INFORMATION: C terminal unaltered
19 US-09-485-421-196

```

```

Query Match 40.0% Score 87 108 42 Length 182
Post Local Similarity 100.0% Prod. No. 0.12
Matches 82 Conservative 02 Mismatches 02 Indels 02 Gaps 02
5 ELITEKIN 12
1111111
10 8 ELITEKIN 15

```

```

1  RESULT 9
2  US-09-485-421-196
3  Sequence 196, Application US/09/040996
4  Patent No. 604742
5  GENERAL INFORMATION:
6  APPLICANT: Bassoux, Jean Louis
7  APPLICANT: Sokol, Renato
8  APPLICANT: Butnot, Klaus
9  APPLICANT: Coruza, Isabelle
10 APPLICANT: Molz, Gunter
11 TITLE OF INVENTION: APO-LIPROTEIN A-1 AGONISTS
12 NUMBER OF SEQUENCES: 254
13 CORRESPONDENCE ADDRESS:
14 ADDRESSEE: Bonito & Edwards LLP
15 STREET: 1155 Avenue of the Americas
16 CITY: New York
17 STATE: NY
18 COUNTRY: USA
19 ZIP: 10046-2811
20 COMPUTER READABLE FORM:
21 MEDIUM TYPE: Diskette
22 COMPUTER: IBM Compat 486
23 OPERATING SYSTEM: DOS
24 SOFTWARE: FASTSEQ Version 2.00
25 CURRENT APPLICATION DATA:
26 FILING DATE: 29 SEP 1997
27 CLASSIFICATION: 911
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER:
30 FILING DATE:
31 ATTORNEY/AGENT INFORMATION:
32 NAME: CORUZZI, Laura A
33 REGISTRATION NUMBER: 40,742
34 REFERENCE/KEY NUMBER: 009196-0006 999
35 TELECOMMUNICATION INFORMATION:
36 TELEPHONE: 650-493-4945
37 TELEFAX: 650-493-5556
38 TELETEXT: 66141 PENNIE
39 INFORMATION FOR SEQ ID NO: 196:
40 SEQUENCE CHARACTERISTICS:

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LENGTH: 18 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 60461660
FEATURE:
LOCATION: 1...18
OTHER INFORMATION: N-terminal acetylated and
OTHER INFORMATION: C-terminal amidated
US-08-940-096-196

Query Match 40.0%; Score 8; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ELLEELKN 12
|||||
DB 8 ELLEELKN 15

RESULT 10
US-08-940-095-253
Sequence 253; Application: US/08940095
Patent No. 6004925

GENERAL INFORMATION:
APPLICANT: Dassau, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Butner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Diouf, Jean
TITLE OF INVENTION: APPLICATION OF A T-CELLS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESS: Penite & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 29-SEP-1997
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: Cornuzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/SEQ ID NO: 253
TELEPHONE: 650-493-4945
TELEFAX: 650-493-4945
FAX: 6641 PENNIE
INFORMATION FOR SEQ ID NO: 253:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 60949250
FEATURE:
NAME/KEY: other
LOCATION: 1...16
OTHER INFORMATION: C-terminal amidated
US-08-940-094-253

OTHER INFORMATION: N-terminal acetylated and
OTHER INFORMATION: C-terminal amidated
US-08-940-095-253

Query Match 25.0%; Score 7; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.76;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ELLEELK 11
|||||
DB 8 ELLEELK 14

RESULT 11
US-08-940-093-253
Sequence 253; Application: US/08940093
Patent No. 6037423

GENERAL INFORMATION:
APPLICANT: Dassau, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Butner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Diouf, Jean
TITLE OF INVENTION: APPLICATION OF A T-CELLS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESS: Penite & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 29-SEP-1997
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cornuzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/SEQ ID NO: 253
TELEPHONE: 650-493-4945
TELEFAX: 650-493-4945
FAX: 6641 PENNIE
INFORMATION FOR SEQ ID NO: 253:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 60374230
FEATURE:
NAME/KEY: other
LOCATION: 1...16
OTHER INFORMATION: N-terminal acetylated and
OTHER INFORMATION: C-terminal amidated
US-08-940-094-253

57 5 ELITEK 11
111111
140 8 ELITEK 11

RESULT 14
US-09-940-095-191

Sequence 192: Application US/0940095
Patent No. 600426

GENERAL INFORMATION:

APPLICANT: Dassau, Jean-Louis

APPLICANT: Sekul, Renato

APPLICANT: Buttner, Klaus

APPLICANT: Court, Isabelle

APPLICANT: Metz, Gunter

TITLE OF INVENTION: ANTIPROTEIN A-1 ANTIBODIES

NUMBER OF INVENTION: AND THEIR USE TO TREAT DYSPLASMIC DISORDERS

ADDRESS: 1155 Avenue of the Americas

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10046-2011

COMPUTER RELEVABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSP Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/940,095

FILING DATE: 29 SEP 1997

CLASSIFICATION: G06

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Court, Laura A

REFERENCE/WORK NUMBER: 009196-0004-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650 493 4935

TELEFAX: 650 493 4935

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 191:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: amino acid

STRANDEDNESS: single

Topology: linear

MULTIPLE TYPE: No, multiple

FEATURE:

NAME/KEY: other

LOCATION: 1...18

OTHER INFORMATION: N-terminal acetylated and

OTHER INFORMATION: C-terminal amidated

US-09-940-095-191

Query Match: 0.08, Score 7, 106 41, Length 18

Best Local Similarity: 100.0%; Prod. No. 0.067

Matches: 7; Conserved type 0; Mismatch class 0; Indels 0; Gaps 0

5 ELITEK 11

111111

8 ELITEK 11

RESULT 14

US-09-940-095-191

Sequence 192: Application US/0940095

Patent No. 600426

GENERAL INFORMATION:

APPLICANT: Dassau, Jean-Louis

APPLICANT: Sekul, Renato

APPLICANT: Buttner, Klaus

APPLICANT: Court, Isabelle

APPLICANT: Metz, Gunter

TITLE OF INVENTION: ANTIPROTEIN A-1 ANTIBODIES

GENERAL INFORMATION:

APPLICANT: Dassau, Jean-Louis

APPLICANT: Sekul, Renato

APPLICANT: Buttner, Klaus

APPLICANT: Court, Isabelle

APPLICANT: Metz, Gunter

TITLE OF INVENTION: ANTIPROTEIN A-1 ANTIBODIES

NUMBER OF INVENTION: AND THEIR USE TO TREAT DYSPLASMIC DISORDERS

ADDRESS: 1155 Avenue of the Americas

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10046-2011

COMPUTER RELEVABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSP Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/940,095

FILING DATE: 29 SEP 1997

CLASSIFICATION: G14

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Court, Laura A

REFERENCE/WORK NUMBER: 009196-0004-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650 493 4935

TELEFAX: 650 493 4935

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 191:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: amino acid

STRANDEDNESS: single

Topology: linear

MULTIPLE TYPE: No, multiple

FEATURE:

NAME/KEY: other

LOCATION: 1...18

OTHER INFORMATION: N-terminal acetylated and

OTHER INFORMATION: C-terminal amidated

US-09-940-095-191

Query Match: 0.08, Score 7, 106 41, Length 18

Best Local Similarity: 100.0%; Prod. No. 0.067

Matches: 7; Conserved type 0; Mismatch class 0; Indels 0; Gaps 0

5 ELITEK 11

111111

8 ELITEK 14

RESULT 14

US-09-940-095-192

Sequence 192: Application US/0940095

Patent No. 600426

GENERAL INFORMATION:

APPLICANT: Dassau, Jean-Louis

APPLICANT: Sekul, Renato

APPLICANT: Buttner, Klaus

APPLICANT: Court, Isabelle

APPLICANT: Metz, Gunter

TITLE OF INVENTION: ANTIPROTEIN A-1 ANTIBODIES

FILE OF INVENTION AND THEIR USE TO TREAT LYSIPHILIC DISORDERS
 NUMBER OF SEQUENCES: 258
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Penno & Edmonds LLP
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10036-2811
 COMPUTER READABLE FORM:
 MEDIUM TYPE: diskette
 COMPUTER: IBM compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 09/094,095
 FILING DATE: 29-SEP-1997
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Cornuzzi, Laura A
 REGISTRATION NUMBER: 30,742
 REFERENCE/EXCERPT NUMBER: 09/106,004-999
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-493-4935
 TELEFAX: 650-493-5556
 TEXT: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 193:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULAR TYPE: NO: 60049250
 FEATURE:
 NAME/KEY: other
 LOCATION: 1...18
 OTHER INFORMATION: N-terminal acetylated and
 OTHER INFORMATION: C-terminal amidated
 US-08-940-095-192

Query Match 35.0% Score 7: DB 3: Length 18:
 Best Local Similarity: 100.0% Pval: No: 0.85:
 Matches 7: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 5 ELLEFLK 11
 DB 8 ELLEFLK 14

RESULT 15
 US-08-940-095-193
 Sequence 193, Application US/08940095
 Patent No. 6004925
 GENERAL INFORMATION:
 APPLICANT: Lassoux, Jean-Louis
 APPLICANT: Sakai, Renate
 APPLICANT: Butner, Klaus
 APPLICANT: Cornuz, Isabelle
 APPLICANT: Metz, Gunder
 APPLICANT: Butner, Jean
 TITLE OF INVENTION: ADOLIPORIN A-1 ANIONISTS
 TITLE OF INVENTION: AND THEIR USE TO TREAT LYSIPHILIC DISORDERS
 NUMBER OF SEQUENCES: 258
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Penno & Edmonds LLP
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: NY
 COUNTRY: USA

ZIP: 10036-2811
 COMPUTER READABLE FORM:
 MEDIUM TYPE: diskette
 COMPUTER: IBM compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 09/094,095
 FILING DATE: 29-SEP-1997
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Cornuzzi, Laura A
 REGISTRATION NUMBER: 30,742
 REFERENCE/EXCERPT NUMBER: 09/106,004-999
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-493-4935
 TELEFAX: 650-493-5556
 TEXT: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 193:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULAR TYPE: NO: 60049250
 FEATURE:
 NAME/KEY: other
 LOCATION: 1...18
 OTHER INFORMATION: N-terminal acetylated and
 OTHER INFORMATION: C-terminal amidated
 US-08-940-095-193

Query Match 35.0% Score 7: DB 3: Length 18:
 Best Local Similarity: 100.0% Pval: No: 0.85:
 Matches 7: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 5 ELLEFLK 11
 DB 8 ELLEFLK 14

Search completed: October 3, 2001, 17:27:46
 Job time: 124 sec

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us protein - protein search, using sw model

Run on: October 4, 2001, 13:24:32 : Search time 22.56 seconds
(without alignments)
67.531 Million cell updates/sec

Title: us-09-485-421-1_copy_17_36

Feature score: 29

Sequence: 1 WTELELLKKNVAVHPPR 20

Scoring table: gapop 60.0 / capext 60.0

Searched: 219241 seqs, 76174552 residues

Word size: 0

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum PP seq length: 20000000

Post-processing: listing first 45 summaries

Database: 1: PIR_68**
2: PIR1**
3: PIR2**
4: PIR3**
5: PIR4**

Prod No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match	Length	PP	IP	Description
1	19	95.0	96	2	109444	VPR protein - huma
2	14	70.0	96	1	ASLJSC	VPR protein - simi
3	10	50.0	96	2	109483	VPR protein - huma
4	10	50.0	96	2	101670	VPR protein - huma
5	10	50.0	96	2	544380	VPR protein - huma
6	10	50.0	97	1	044001	VPR protein - huma
7	8	40.0	623	2	882536	Anc transporter A
8	8	40.0	635	2	561935	Anc transporter A
9	8	40.0	635	2	085621	hypothetical prote
10	8	40.0	635	2	322134	Anc transporter A
11	7	35.0	150	2	871206	probable leucine-r
12	7	35.0	157	2	113461	hypothetical prote
13	7	35.0	222	2	034233	transcription fact
14	7	35.0	295	1	879631	conserved hypotet
15	7	35.0	459	2	864171	Anc type transport
16	7	35.0	471	2	529039	Nu. transporter A
17	7	35.0	542	2	672404	Flavellur B-ring p
18	7	35.0	535	1	149730	NuM dehydrogenase
19	7	35.0	544	2	491144	acetylactate synth
20	7	35.0	640	2	883267	probable ATP-bind
21	7	35.0	647	2	864170	Anc type transport
22	7	35.0	719	2	134090	hypothetical prote
23	7	35.0	968	2	064691	type III resistin
24	7	35.0	972	2	071826	hypothetical prote
25	7	35.0	1005	2	A64465	hypothetical prote
26	7	35.0	1159	2	A64505	hypothetical prote
27	6	30.0	38	2	170014	Kallikrein - mouse
28	6	30.0	52	2	042196	metalloyl aminopep
29	6	30.0	62	2	845283	cal protein phag

ALIGNMENTS

```

RESULT 1
109444
VPR protein - human immunodeficiency virus type 1 (strain JREF)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 16 Jul 1979 *sequence_revision 16 Jul 1979 *ext_change 26-Aug-1999
C:Accession: 109444
E:Yang, S.; Viscusi, R.V.; Abashvili, G.; Johnson, W.A.; Chou, J.S.; Kraybill, J.; Nijm32
submitted to the EMBL Data Library, July 1996
A:Reference number: 216673
A:Accession: 109444
A:Status: Preliminary; translated from CD4/CD8+ T008J
A:Molecule type: DNA
A:Residues: 1-96 (PAM)
A:Cross-references: EMBL:063632; MID:q1465777; PIR:q1465784
C:Genetics:
A:Gene: VPR
C:Superfamily: AIDS VPR protein

Query Match          95.0%  Score 19;  PP 2;  Length 96;
Best Local Similarity 100.0%  Prod. No. 9,8e-12;
Matches 19;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

37  2 WTELELLKKNVAVHPPR 20
db  18 WTELELLKKNVAVHPPR 36

RESULT 2
ASLJSC
VPR protein - simian immunodeficiency virus SIVcpz
M:Alternate names: orf-R protein
C:Species: Simian immunodeficiency virus SIVcpz
A:Note: Host Pan troglodytes (chimpanzee)
C:Date: 30 Sep 1991 *sequence_revision 30-Sep-1991 *ext_change 16-Jul-1999
C:Accession: S09986
E:Ruetz, T.; Geyer, R.; Meyerhans, A.; Roelants, G.; Wain Hosen, S.;
Nature 345, 356-359, 1990
A>Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.
A:Reference number: S09983; MID:q025077
A:Accession: S09986
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-96 (HIV)
A:Cross-references: EMBL:X52154, MID:q56866, FID:GMA5403.1; PIR:q56870
C:Genetics:
A:Gene: vpr
C:Superfamily: AIDS VPR protein
C:Keywords: AIDS, immunodeficiency

Query Match          70.0%  Score 14;  PP 1;  Length 96;

```


Wed Oct 3 13:40:07 2001

us-09-485-421-1_copy_17_36.rpr

Page 5

Search completed: October 3, 2001, 13:29:03
Job time: 271 sec

•

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GenCore version 4.5
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GM protein - protein search using sw model

Run on: October 3, 2001, 13:25:22; Search time 34.22 seconds
(without alignments)
76.415 Million cell updates/sec

Title: US-09-485-421-1_COPY_17_36

Perfect score: 20

Sequence: 1 MWTELELEKKNVAVHPPR 20

Scoring table:

Gapop 60.0, Gapext 60.0

Searched: 425926 seqs, 13205027 residues

Word size: 0

Total number of hits satisfying chosen parameters: 425926

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

Database: 1: SP archaea: *
2: SP bacteria: *
3: SP fungi: *
4: SP human: *
5: SP invertebrate: *
6: SP mammal: *
7: SP mpo: *
8: SP organelle: *
9: SP phage: *
10: SP plant: *
11: SP rodent: *
12: SP unclassified: *
13: SP vertebrate: *
14: SP virus: *

Prod. Rev. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the entire database.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Accession
1	20	100.0	95	14	Q9E208 human immun
2	20	100.0	96	14	Q9E208 human immun
3	20	100.0	96	14	Q9E208 human immun
4	20	100.0	96	14	Q9E208 human immun
5	19	95.0	37	14	Q9E208 human immun
6	19	95.0	67	14	Q9E208 human immun
7	19	95.0	93	14	Q9E208 human immun
8	19	95.0	94	14	Q9E208 human immun
9	19	95.0	94	14	Q9E208 human immun
10	19	95.0	94	14	Q9E208 human immun
11	19	95.0	94	14	Q9E208 human immun
12	19	95.0	94	14	Q9E208 human immun
13	19	95.0	94	14	Q9E208 human immun
14	19	95.0	94	14	Q9E208 human immun
15	19	95.0	94	14	Q9E208 human immun
16	19	95.0	94	14	Q9E208 human immun
17	19	95.0	94	14	Q9E208 human immun
18	19	95.0	94	14	Q9E208 human immun
19	19	95.0	94	14	Q9E208 human immun
20	19	95.0	94	14	Q9E208 human immun

20	19	95.0	95	14	Q9E208 human immun
21	19	95.0	95	14	Q9E208 human immun
22	19	95.0	95	14	Q9E208 human immun
23	19	95.0	95	14	Q9E208 human immun
24	19	95.0	95	14	Q9E208 human immun
25	19	95.0	95	14	Q9E208 human immun
26	19	95.0	95	14	Q9E208 human immun
27	19	95.0	95	14	Q9E208 human immun
28	19	95.0	95	14	Q9E208 human immun
29	19	95.0	95	14	Q9E208 human immun
30	19	95.0	95	14	Q9E208 human immun
31	19	95.0	95	14	Q9E208 human immun
32	19	95.0	95	14	Q9E208 human immun
33	19	95.0	95	14	Q9E208 human immun
34	19	95.0	95	14	Q9E208 human immun
35	19	95.0	95	14	Q9E208 human immun
36	19	95.0	95	14	Q9E208 human immun
37	19	95.0	95	14	Q9E208 human immun
38	19	95.0	95	14	Q9E208 human immun
39	19	95.0	95	14	Q9E208 human immun
40	19	95.0	95	14	Q9E208 human immun
41	19	95.0	95	14	Q9E208 human immun
42	19	95.0	95	14	Q9E208 human immun
43	19	95.0	95	14	Q9E208 human immun
44	19	95.0	95	14	Q9E208 human immun
45	19	95.0	95	14	Q9E208 human immun

ALIGNMENTS

RESULT 1	036208	PRELIMINARY	PRT	96 AA
AC	036208			
DT	01-JAN-1998 (TREMUR1.05, Created)			
DT	01-JAN-1998 (TREMUR1.05, Last sequence update)			
DT	01 MAY 2000 (TREMUR1.13, Last annotation update)			
DE	VPR PROTEIN.			
GN	VPR.			
OS	Human immunodeficiency virus type 1.			
OC	Viruses; Retroviridae; Retroviridae; Lentiviridae.			
OX	NCBI_TaxID:11676;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Song J., Wang B., Ge Y.C., Taylor D., Dowton D., Cunningham A.,			
RA	Sakuma N.			
EC	3.6.1.1 (ATC 1.9.7) 1. 1b. HIV-1 Gag polyprotein p170-175.			
DR	EMBL: AF000322; AAB70161.1; -			
DR	InterPro: IPR000012; -			
DR	PIR: P00522; VPR; 1.			
DR	PRINTS: PR00444; HIVPRVPR.			
SC	SPRINGER: 96 AA; 11353 RMS; 628725A266994D; CR064;			
Query Match	100.0%	Score 20	DB 14	Length 96;
Best Local Similarity	100.0%	Prod. No. 75e11;		
Matches 20	Characteristics 0	Mismatches 0	Indels 0	Gaps 0;
Cy	1 MWTELELEKKNVAVHPPR 20			
DB	11111111111111111111			
DB	17 MWTELELEKKNVAVHPPR 36			
RESULT 2	073369	PRELIMINARY	PRT	96 AA
AC	073369			
DT	01-NOV-1996 (TREMUR1.01, Created)			
DT	01-NOV-1996 (TREMUR1.01, Last sequence update)			
DT	01 MAY 2000 (TREMUR1.13, Last annotation update)			
DE	VPR PROTEIN.			
GN	VPR.			

[illegible][illegible]

RESULT	4		
Q91092			
ID	Q91092	PRELIMINARY:	PRT: 96 AA.
AC	Q91092;		
DI	01-Oct-2000 (IEMBL01, 15, Created)		
DT	01-Oct-2000 (IEMBL01, 15, last sequence update)		
PR	01-Mar-2001 (IEMBL01, 16, last annotation update)		
DE	VPR, PROTEIN.		
GN	VPR.		
OS	Human immunodeficiency virus type 1.		
OC	Viruses; Retroviruses; Retroviridae; Lentivirus.		
OX	NCBI_TaxID:11676;		
RD	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-PATENT 18;		
PX	MEP1.NE-20348/96; PubMed 1081687;		
RA	Yamada T., Iwamoto A.;		
RT	"Comparison of proviral accessory genes between long-term		
RT	nonprogressors and progressors of human immunodeficiency virus type 1		
RI	infection.";		
RL	Arch. Virol. 145:1021-1027(2000).		
EMBL	AF034554; FAA94601.1; -;		
DB	InterPro: IPR000112; -;		
DB	InterPro: IPR001591; -;		
DB	PIfam: PF005522; VPR; 1.		
DB	PRINTS: PR00444; HIVVPRVX.		
DB	Proteome: IP001667; -; 1.		
SD	SEQUENCE 96 AA: 11306 MW: 407137E8584E7E0 CAC64;		

```

Query Match: 100.0%; Score 20; DB 14; Length 96;
Host: Local SimBar14; 100.0%; Eval. No. 7 5e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TWTELEEEHKNEAVRPPR 20
      | | | | | | | | | | | | | | | | | | | | | |
DB 17 TWTELEEEHKNEAVRPPR 36

RESULT 5
ID O89598 PRELIMINARY: PRT: 37 AA.
AC O89598;
DE 01-NOV-1996 (TEMBREL, 01, Created)
DI 01-NOV-1996 (TEMBREL, 01, Last sequence update)
DI 01-MAY-2000 (TEMBREL, 13, Last annotation update)
DE HIV-1 DNA FOR GAG, POL, VIF, VIFR, REV, TAT, ENV, VIF,
VPR.
OS Human immunodeficiency virus type 1.
GX Viruses; Retroid viruses; Retroviridae; Lentiviruses.
GX NCBI:taxid:11676;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN-EM213;
RA Lloyd M.W., Moore B.E.;
RL Submitted (JUN 1996) to the EMBL/GenBank/JNBRJ databases.
RN 121
RP SEQUENCE FROM N.A.
RC STRAIN-EM213;
RA Lattat V.;
RL Submitted (JUN 1996) to the EMBL/GenBank/JNBRJ databases.
DB EMBL: D86066; PAA1299.1; ;
DB EMBL: D86068; PAA1299.1; ;
DB FofrPro: FPRO0012;
DB Pfam: PF00522; VIF_1;
DE FUSEINTE 37 AA; 448 MB; 410700048735277 chr64;

```

Query Match	95.08; Score 19; Bits 14; Length 47;
Best Local Similarity	100.08; Prod. No. 2, 5e-10;
Matches	19; Conservative 0; Mismatches 0; Gaps 0;

DB 18 WTLLELEKNEAVRHP 46

RESULT 11
ID 079268 PRELIMINARY PRT: 95 AA.
AC 079268
DT 01-MAY-2000 (ITEMBROL: 15, last sequence update)
DE 01-MAY-2000 (ITEMBROL: 15, last annotation update)
CN VPR PROTEIN (FRAGMENT).
OS Human immunodeficiency virus type 1.
CA Viruses; Retroviruses; Retroviridae; Lentiviruses.
GX NBL_FOLD-116762
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN MN13.13
KA Aboud N., Yoshida H., V. S. B. K.
KL Basic characterization of functional domains of human immunodeficiency virus type 1 vif and vpr genes correlated with lack of vortical transmission.
RL Submitted (09N-2000) to the EMBL/Genbank/Tran database.
RE EMBL: AF256093; AA:32257.1;
FI N-138 94
SO SHODENSE 94 AA: 11150 MW: 18000p254021670 CR664;

Query Match 95.0% Score 19; DR 14; Length 95;
Best Local Similarity 100.0% Prod. No. 5,60-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 18 WTLLELEKNEAVRHP 46

RESULT 11
ID 079268 PRELIMINARY PRT: 95 AA.
AC 079268
DT 01-MAY-1998 (ITEMBROL: 07, created)
DT 01-MAY-1998 (ITEMBROL: 07, last sequence update)
DT 01-MAY-2000 (ITEMBROL: 15, last annotation update)
DE PARIAVIRUS (VIRUS) (VIRUS) (VIRUS) (VIRUS)
CN VPR.
OS Human immunodeficiency virus type 1.
CA Viruses; Retroviruses; Retroviridae; Lentiviruses.
GX NBL_FOLD-116762
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN L.N.E.
KA Nureki P., Bousso P., Courtillot C., Parnet-Mathieu F., Bousso P.,
KL Basic characterization of functional domains of human immunodeficiency virus type 1 vif and vpr genes correlated with lack of vortical transmission.
RL Submitted (09V-1998) to the EMBL/Genbank/Tran database.
RE EMBL: Z68127; CA:07096.1;
FI 100 95
SO SHODENSE 95 AA: 11264 MW: 18000p254021670 CR664;

Query Match 95.0% Score 19; DR 14; Length 95;
Best Local Similarity 100.0% Prod. No. 5,60-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 18 WTLLELEKNEAVRHP 46

RESULT 12

ID 079264 PRELIMINARY PRT: 95 AA.
AC 079264
DT 01-NOV-1996 (ITEMBROL: 01, created)
DT 01-NOV-1996 (ITEMBROL: 01, last sequence update)
DT 01-MAY-2000 (ITEMBROL: 15, last annotation update)
CN VPR PROTEIN.
OS Human immunodeficiency virus type 1.
CA Viruses; Retroviruses; Retroviridae; Lentiviruses.
GX NBL_FOLD-116762
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN PATIENT 0033, IV DRUG USER, DUTCH;
KA Kalkon L., Courtillot C., Zouharat F., Hartman S., Gibbs J.,
KL Goldsmith J.
RL J. Gen. Virol. 0:0 0(1996).
RE EMBL: Z68567; CA:92891.1;
DE InterPro: IPR00012;
DR PRIME: PR00522; VPR: 1
DE PRINTS: PR00444; HIVVPRVX.
SO SHODENSE 95 AA: 11313 MW: 18000p254021670 CR664;

Query Match 95.0% Score 19; DR 14; Length 95;
Best Local Similarity 100.0% Prod. No. 5,70-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 18 WTLLELEKNEAVRHP 46

RESULT 13
ID 079268 PRELIMINARY PRT: 95 AA.
AC 079268
DT 01-NOV-1996 (ITEMBROL: 01, created)
DT 01-NOV-1996 (ITEMBROL: 01, last sequence update)
DT 01-MAY-2000 (ITEMBROL: 15, last annotation update)
DE VPR PROTEIN.
CN VPR.
OS Human immunodeficiency virus type 1.
CA Viruses; Retroviruses; Retroviridae; Lentiviruses.
GX NBL_FOLD-116762
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN PATIENT 0221, IV DRUG USER, DUTCH;
KA Kalkon L., Courtillot C., Zouharat F., Hartman S., Gibbs J.,
KL Goldsmith J.
RL J. Gen. Virol. 0:0 0(1996).
RE EMBL: Z68571; CA:92895.1;
DE InterPro: IPR00012;
DR PRIME: PR00522; VPR: 1
DE PRINTS: PR00444; HIVVPRVX.
SO SHODENSE 95 AA: 11116 MW: 18000p254021670 CR664;

Query Match 95.0% Score 19; DR 14; Length 95;
Best Local Similarity 100.0% Prod. No. 5,70-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 18 WTLLELEKNEAVRHP 46

RESULT 14
ID 079281 PRELIMINARY PRT: 95 AA.
AC 079281
DT 01-NOV-1996 (ITEMBROL: 01, created)

Example: Fig 1b: 64pp: English.

The present invention describes a conjugate composition comprising a fragment of HIV-1 or non-HIV-1 Vpr protein conjugated to a therapeutic compound. The compound can be used in a method for inhibiting cell proliferation. It can also be used for treating an individual who has a hyperproliferative disease. The HIV-1 Vpr or non-HIV-1 Vpr protein fragments can be used for identifying compounds that inhibit Vpr protein binding to the p6 domain of p55 or to p6 protein. The present sequence represents an HIV protein sequence.

Sequence: 96 AA:

Query Match: 100.0%; Score: 26; DB: 20; Length: 96;
Best Local Similarity: 100.0%; Pred. No. 8, 2e-19;
Matches: 26; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 ALIRLQGLIFIRICGRSRIGIT 26
DB 59 aIIIRLQGLIFIRICGRSRIGIT 84

RESULT 2

AAW99815: 100.0%; standard: protein; 96 AA:

AAW99815:

08-JUN-1999 (first entry)

HIV-1 Vpr protein.

HIV-1 Vpr: human immunodeficiency virus; hyperproliferative disease;

cell proliferation.

Human immunodeficiency virus type 1.

W090412-AT.

25-FEB-1999.

14-AUG-1998: 98WO-0516890.

14-AUG-1997: 97US-0055754.

(OYPE) HIV-1 PPRNSYLVANIA.

Ayazov V, Kibbet Emmons T, Mahalingam S, Patel M;

Weiner DG;

WPI: 1999-181154/15.

Conjugate composition comprising HIV-1 Vpr protein fragment - used

to inhibit cell proliferation, and treating hyperproliferative

diseases.

Example: Fig 1A: 64pp: English.

The present invention describes a conjugate composition comprising a fragment of HIV-1 or non-HIV-1 Vpr protein conjugated to a therapeutic compound. The compound can be used in a method for inhibiting cell proliferation. It can also be used for treating an individual who has a hyperproliferative disease. The HIV-1 Vpr or non-HIV-1 Vpr protein fragments can be used for identifying compounds that inhibit Vpr protein binding to the p6 domain of p55 or to p6 protein. The present sequence represents a HIV-1 Vpr protein sequence.

Sequence: 96 AA:

Query Match: 100.0%; Score: 26; DB: 20; Length: 96;
Best Local Similarity: 100.0%; Pred. No. 8, 2e-19;

Matches: 26; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 ALIRLQGLIFIRICGRSRIGIT 26
DB 59 aIIIRLQGLIFIRICGRSRIGIT 84

RESULT 4

AAW99815: 100.0%; standard: protein; 96 AA:

AAW99815:

08-JUN-1999 (first entry)

HIV Vpr wt protein sequence.

HIV-1 Vpr: human immunodeficiency virus; hyperproliferative disease;

cell proliferation.

Human immunodeficiency virus.

W9909412-AT.

25-FEB-1999.

14-AUG-1998: 98WO-0516890.

14-AUG-1997: 97US-0055754.

(OYPE) HIV-1 PPRNSYLVANIA.

Ayazov V, Kibbet Emmons T, Mahalingam S, Patel M;

Weiner DG;

WPI: 1999-181154/15.

Conjugate composition comprising HIV-1 Vpr protein fragment - used

to inhibit cell proliferation, and treating hyperproliferative

diseases.

Example: Fig 1b: 64pp: English.

The present invention describes a conjugate composition comprising a fragment of HIV-1 or non-HIV-1 Vpr protein conjugated to a therapeutic compound. The compound can be used in a method for inhibiting cell proliferation. It can also be used for treating an individual who has a hyperproliferative disease. The HIV-1 Vpr or non-HIV-1 Vpr protein fragments can be used for identifying compounds that inhibit Vpr protein binding to the p6 domain of p55 or to p6 protein. The present sequence represents an HIV protein sequence.

Sequence: 96 AA:

Query Match: 100.0%; Score: 26; DB: 20; Length: 96;
Best Local Similarity: 100.0%; Pred. No. 8, 2e-19;
Matches: 26; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 ALIRLQGLIFIRICGRSRIGIT 26
DB 59 aIIIRLQGLIFIRICGRSRIGIT 84

RESULT 4

AAW99815: 100.0%; standard: protein; 96 AA:

AAW99815:

08-JUN-1999 (first entry)

HIV E21, 24P protein sequence.

```

XX HIV Vpr: human immunodeficiency virus; hyperproliferative disease;
FM cell proliferation.
KM
XX Human immunodeficiency virus.
GS
XX W69909412-A1.
FM
XX 25-FEB-1999.
PD
XX
XX 14-AUG-1998; 98WO-0516890.
XX
XX 14-AUG-1997; 97US-0055754.
XX
XX (UNPE-) UNIV PENNSYLVANIA.
PA
XX
XX Ayyavoo V, Kieber Emmens T, Mahalingam S, Patel M,
PI Weiner DB;
XX WPI: 1999-181154/15.
XX
XX Conjugate composition comprising HIV-1 Vpr protein fragment - used
PI to inhibit cell proliferation, and treating hyperproliferative
PT diseases
XX
XX Example: Fig 1B, 64pp; English
XX
XX The present invention describes a conjugate composition comprising a
CC fragment of HIV-1 or non-HIV-1 Vpr protein conjugated to a therapeutic
CC compound. The conjugate can be used in a method for inhibiting cell
CC proliferation. It can also be used for treating an individual who has a
CC hyperproliferative disease. The HIV-1 Vpr or non-HIV-1 Vpr protein
CC fragments can be used for identifying compounds that inhibit Vpr protein
CC binding to the p6 domain of p55 or to p6 protein. The present sequence
CC represents an HIV protein sequence.
XX
XX Sequence 96 AA:
SQ
Query Match: 100.0%; Score 26; DB 20; Length 96;
Host Local Similarity 100.0%; Pred. No. 8, 2e-19;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALIRIQGLIFHRIQGRSRIGII 26
DB 59 ALIRIQGLIFHRIQGRSRIGII 84
RESULTS 5
AAW99817
ID AAW99817 standard; protein; 96 AA.
XX
XX AAW99817;
AC
XX 08-JUN-1999 (first entry)
XX
XX HIV alpha-A protein sequence.
DE
XX HIV Vpr: human immunodeficiency virus; hyperproliferative disease;
FM cell proliferation.
KM
XX Human immunodeficiency virus.
GS
XX W69909412-A1.
FM
XX 25-FEB-1999.
PD
XX
XX 14-AUG-1998; 98WO-0516890.
XX
XX 14-AUG-1997; 97US-0055754.
XX
XX (UNPE-) UNIV PENNSYLVANIA.
PA
XX

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FI Ayyavoo V, Kieber Emmens T, Mahalingam S, Patel M,
FI Weiner DB;
XX WPI: 1999-181154/15.
XX
XX Conjugate composition comprising HIV-1 Vpr protein fragment - used
XX to inhibit cell proliferation, and treating hyperproliferative
XX diseases
XX
XX Example: Fig 1B, 64pp; English.
XX
XX The present invention describes a conjugate composition comprising a
CC fragment of HIV-1 or non-HIV-1 Vpr protein conjugated to a therapeutic
CC compound. The conjugate can be used in a method for inhibiting cell
CC proliferation. It can also be used for treating an individual who has a
CC hyperproliferative disease. The HIV-1 Vpr or non-HIV-1 Vpr protein
CC fragments can be used for identifying compounds that inhibit Vpr protein
CC binding to the p6 domain of p55 or to p6 protein. The present sequence
CC represents an HIV protein sequence.
XX
XX Sequence 96 AA:
SQ
Query Match: 100.0%; Score 26; DB 20; Length 96;
Host Local Similarity 100.0%; Pred. No. 8, 2e-19;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALIRIQGLIFHRIQGRSRIGII 26
DB 59 ALIRIQGLIFHRIQGRSRIGII 84
RESULTS 6
AAW99818
ID AAW99818 standard; protein; 96 AA.
XX
XX AAW99818;
AC
XX 08-JUN-1999 (first entry)
XX
XX HIV A30S protein sequence.
DE
XX HIV Vpr: human immunodeficiency virus; hyperproliferative disease;
FM cell proliferation.
KM
XX Human immunodeficiency virus.
GS
XX W69909412-A1.
FM
XX 25-FEB-1999.
PD
XX
XX 14-AUG-1998; 98WO-0516890.
XX
XX 14-AUG-1997; 97US-0055754.
XX
XX (UNPE-) UNIV PENNSYLVANIA.
PA
XX
XX Ayyavoo V, Kieber Emmens T, Mahalingam S, Patel M,
PI Weiner DB;
XX WPI: 1999-181154/15.
XX
XX Conjugate composition comprising HIV-1 Vpr protein fragment - used
XX to inhibit cell proliferation, and treating hyperproliferative
XX diseases
XX
XX Example: Fig 1B, 64pp; English.
XX
XX The present invention describes a conjugate composition comprising a
CC fragment of HIV-1 or non-HIV-1 Vpr protein conjugated to a therapeutic
CC compound. The conjugate can be used in a method for inhibiting cell
CC proliferation. It can also be used for treating an individual who has a
CC hyperproliferative disease. The HIV-1 Vpr or non-HIV-1 Vpr protein
CC fragments can be used for identifying compounds that inhibit Vpr protein
CC binding to the p6 domain of p55 or to p6 protein. The present sequence
CC represents an HIV protein sequence.
XX

```

The present invention can be used for identifying compounds that inhibit Vpr protein binding to the p6 domain of p55 or to p6 protein. The present sequence represents an HIV protein sequence.

Sequence: 96 AA:

Query Match: 100.0% Score: 25; ID: 20; Length: 96;
 Best Local Similarity: 100.0% Prod. No. 8, 26-19;
 Matches: 25; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
 1 ALPHAGALACTOSE-INDUCED
 59 ALPHAGALACTOSE-INDUCED 84

RESULT 7

AAW99819: 100.0% Score: 25; ID: 20; Length: 96;
 Best Local Similarity: 100.0% Prod. No. 8, 26-19;
 Matches: 25; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

AAW99819:

08-JUN-1999 (first entry)

HIV ASOL protein sequence.

HIV Vpr: human immunodeficiency virus; hyperproliferative disease;

cell proliferation.

Human immunodeficiency virus.

W0990412-A1.

25-FEB-1999.

14-AUG-1998: 98WC-US1690.

14-AUG-1997: 97US-0055754.

(TYPE-) UNIV PENNSYLVANIA.

AYYAYOO V, Kleber-Emons T, Mahalingam S, Patel M;

Wolner DB;

WPI: 1999-181154/15.

Conjugate composition comprising HIV-1 Vpr protein fragment used

to inhibit cell proliferation and treat hyperproliferative

diseases.

Example: FIG 1B, 64pp; English.

The present invention describes a conjugate composition comprising a

fragment of HIV-1 or non-HIV-1 Vpr protein conjugated to a therapeutic

compound. The compound can be used in a method for inhibiting cell

proliferation. It can also be used for treating an individual who has a

hyperproliferative disease. The HIV-1 Vpr or non-HIV-1 Vpr protein

fragments can be used for identifying compounds that inhibit Vpr protein

binding to the p6 domain of p55 or to p6 protein. The present sequence

represents an HIV protein sequence.

Sequence: 96 AA:

Query Match: 100.0% Score: 25; ID: 20; Length: 96;

Best Local Similarity: 100.0% Prod. No. 8, 26-19;

Matches: 25; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

1 ALPHAGALACTOSE-INDUCED

59 ALPHAGALACTOSE-INDUCED 84

RESULT 8

AAW99820: 100.0% Score: 25; ID: 20; Length: 96;

Best Local Similarity: 100.0% Prod. No. 7, 9e-18;

Matches: 25; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

20-APR-2001 (first entry)

HIV ASOL protein sequence.

HIV Vpr: human immunodeficiency virus; hyperproliferative disease;

cell proliferation.

Human immunodeficiency virus.

W0990412-A1.

25-FEB-1999.

14-AUG-1998: 98WC-US1690.

14-AUG-1997: 97US-0055754.

(TYPE-) UNIV PENNSYLVANIA.

AYYAYOO V, Kleber-Emons T, Mahalingam S, Patel M;

Wolner DB;

WPI: 1999-181154/15.

Conjugate composition comprising HIV-1 Vpr protein fragment used

to inhibit cell proliferation and treating hyperproliferative

diseases.

Example: FIG 1B, 64pp; English.

The present invention describes a conjugate composition comprising a

fragment of HIV-1 or non-HIV-1 Vpr protein conjugated to a therapeutic

compound. The compound can be used in a method for inhibiting cell

proliferation. It can also be used for treating an individual who has a

hyperproliferative disease. The HIV-1 Vpr or non-HIV-1 Vpr protein

fragments can be used for identifying compounds that inhibit Vpr protein

binding to the p6 domain of p55 or to p6 protein. The present sequence

represents an HIV protein sequence.

Sequence: 96 AA:

Query Match: 100.0% Score: 25; ID: 20; Length: 96;

Best Local Similarity: 100.0% Prod. No. 7, 9e-18;

Matches: 25; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

20-APR-2001 (first entry)

HIV-1 non-subtype B clone 94HR020-1 Vpr protein.

HIV-1: human immunodeficiency virus; non subtype B gag, pol, env;

vpr; vif; vpr; tat; rev; act; vaccine.

Human immunodeficiency virus type 1.

W0990412-A1.

Best Local Similarity 100.0%; Prod. No. 7.2e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRLIQLLPFHPRIGCRHSRIQ 24
ID 61 IRLIQLLPFHPRIGCRHSRIQ 82

RESULT 14

AAM53040
ID AAM53040 standard; peptide: 96 AA.

AC AAM53040;

DT 17-JUL-1998 (first entry)

DE HIV-1 polypeptide.

KM Recombinant plant virus; HIV-1; protein production; immunisation;
KM fusion capsid protein; alpha mosaic virus; flavivirus; pathogen;
KM rhadovirus.

OS Human immunodeficiency virus type 1

PN W09808375-A1.

PD 05-MAR-1998.

PE 28-AUG-1997; 92MO-0815200

PP 28-AUG-1998; 92MO-074456

PA (UNLDE-) UNIV JEFFERSON THOMAS.

PI Hooper DC; Koprowski H; Medelska A; Yushov V;

DK WPI: 1998-179070/16.

PT Production of HIV-1 polypeptides, particularly for use in vaccine, by
PT expression as fusion proteins with plant virus capsid proteins in
PI plant cells infected with virus

PS Disclosure: Page 4; 42FF; English.

CC This sequence is a HIV-1 polypeptide that can be used in a recombinant
CC plant virus used in the process of the invention. The process is for
CC administering a polypeptide to an animal comprising: (a) infecting a
CC plant cell with recombinant plant virus nucleic acid that will be
CC processed in a plant cell to produce a fusion capsid protein (FVP), the
CC FVP comprises a plant virus capsid protein (VCP) and a polypeptide that
CC is not a VCP, the FVP being an alpha mosaic virus (AMV) capsid
CC protein (CP) or flavivirus CP thereby creating a infected cell;
CC (b) culturing the infected cell, or a derivative cell derived from the
CC infected cell, under conditions where the infected cell or derivative
CC cell makes the FVP, and (c) administering the FVP or a portion to an
CC animal. The recombinant plant virus can also be used for production of
CC polypeptides. The method is used particularly for the production of
CC polypeptides which can be used for immunisation against pathogens such as
CC rhadovirus or HIV.

CC Sequence 96 AA:

Query Match 84.6%; Score 22; DB 19; Length 96;

Best Local Similarity 100.0%; Prod. No. 7.2e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRLIQLLPFHPRIGCRHSRIQ 24

ID 61 IRLIQLLPFHPRIGCRHSRIQ 82

RESULT 15

AAB10685
ID AAB10685 standard; peptide: 96 AA.

AC AAB10685;

DT 19 JAN-2001 (first entry)

DE HIV-1 regulatory virus protein R peptide sVpr1-96.

KM Regulatory virus protein R (Vpr) antiviral gene therapy;
KM pathogenicity; structural analysis; cell cycle arrest.

OS Synthetic.

OS Human immunodeficiency virus type 1.

PN W0200049038-A2.

PD 24-AUG-2000.

PE 19-FEB-2000; 2000W-1000595.

PP 19-FEB-1999; 99DE-1008752.

PA (SCHU/) SCHUBERT U.

PA (HENK/) HENKLEIN P.

PA (WRAV/) WRAV V.

PI Schubert U; Henklein P; Wray V;

DK WPI: 2000-065457/52.

PT New synthetic peptides from the Vpr protein of human immune deficiency
PT virus, useful e.g. for therapy and diagnosis, have good solubility in
PT water.

PS Claim 3.1; Page 5; 35PP; German.

CC This invention describes novel synthetic peptides (1) derived from the
CC regulatory viral protein R (Vpr) of human immunodeficiency virus-1
CC (HIV-1) which have antiviral activity and can be used for gene therapy.
CC (1) is used for therapeutic and/or diagnostic purposes, especially in
CC biological assays, for detection of serological tests, e.g. enzyme linked
CC immunosorbent assays (ELISA) (e.g. for detecting or quantifying Vpr in
CC blood). To raise specific antibodies and antisera (especially those
CC reactive with specific epitopes), and as antiviral agents (1) can also
CC be used in screening for potential Vpr antagonists (i.e. compounds that
CC modulate interaction of Vpr with cellular factors,
CC transcription activating properties of Vpr, transport of Vpr and its
CC incorporation into viral particles, Vpr induced cell cycle arrest, and
CC cytoxic and/or chemotactic activities of Vpr). (1) is used to establish
CC cell or animal models for studying pathogenicity of Vpr, for structural
CC analysis of Vpr and its domains, for in vitro assembly of new vectors
CC for gene therapy. In vitro is used for complementing the function
CC of Vpr derived mutants in cell cultures, and to reduce flexibility of Vpr
CC induced by the R1 domain. Synthetic (1) are soluble in water and
CC can be formulated as highly concentrated solutions (molar) without
CC protein aggregation, so are well suited to analysis by nuclear magnetic
CC resonance, X ray or circular dichroism techniques. (1) adopt a folded
CC structure, have biological activity comparable to that of viral Vpr, and
CC can be produced, at high purity, on the milligram scale. This sequence
CC represents the synthetic HIV-1 derived Vpr peptide sVpr1-96 which is used
CC in the method of the invention.

CC Sequence 96 AA:

Query Match 94.4%; Score 22; DB 21; Length 96;

Best Local Similarity 100.0%; Prod. No. 7.2e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRLIQLLPFHPRIGCRHSRIQ 24

ID 61 IRLIQLLPFHPRIGCRHSRIQ 82

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Page 8

Table 1

Year	Population	GDP	Urbanization	Life expectancy	Fertility rate	Mortality rate	Healthcare expenditure	Education expenditure	Government expenditure
1960	1.2 billion	\$100 billion	20%	47 years	6.5 children/woman	20 per 1,000 live births	\$1 billion	\$2 billion	\$5 billion
1980	1.5 billion	\$300 billion	30%	55 years	4.5 children/woman	15 per 1,000 live births	\$5 billion	\$10 billion	\$15 billion
2000	2.0 billion	\$1 trillion	45%	65 years	2.5 children/woman	10 per 1,000 live births	\$20 billion	\$40 billion	\$60 billion
2020	2.5 billion	\$2.5 trillion	60%	75 years	1.5 children/woman	5 per 1,000 live births	\$100 billion	\$200 billion	\$300 billion

$$\begin{aligned} \text{C}_{10}\text{H}_8\text{O}_2 + \text{C}_6\text{H}_6 &\rightarrow \text{C}_{16}\text{H}_{14}\text{O}_2 + \text{C}_4\text{H}_2 \\ \text{C}_{10}\text{H}_8\text{O}_2 + \text{C}_6\text{H}_6 &\rightarrow \text{C}_{16}\text{H}_{14}\text{O}_2 + \text{C}_4\text{H}_2 + \text{C}_4\text{H}_2 + \text{C}_4\text{H}_2 \\ \text{C}_{10}\text{H}_8\text{O}_2 + \text{C}_6\text{H}_6 &\rightarrow \text{C}_{16}\text{H}_{14}\text{O}_2 + \text{C}_4\text{H}_2 + \text{C}_4\text{H}_2 + \text{C}_4\text{H}_2 + \text{C}_4\text{H}_2 \end{aligned}$$

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MM protein - protein search, using SW Model

Query: us-09-485-421-1_copy_17_36 (without alignment)

Search time: 13.68 seconds
50,000 hits, 0.11 of 100,000

Title: US-09-485-421-1_COPY_17_36

Perfect score: 1 TWLELELELNKNAVHPPR 20

Sequence: 1 TWLELELELNKNAVHPPR 20

Scoring table: gapop 60.0, gapext 60.0

Word size: 0

total number of hits satisfying chosen parameters: 94455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being plotted, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
1	19	95.0	78	1	VPR_HV1B1	P05946	human immun
2	19	95.0	78	1	VPR_HV1B5	P05947	human immun
3	19	95.0	96	1	VPR_HV1B8	P05948	human immun
4	19	95.0	96	1	VPR_HV1B8	P20982	human immun
5	17	85.0	96	1	VPR_HV1M1	P05950	human immun
6	14	78.0	96	1	VPR_HV1C2	P27282	human immun
7	10	50.0	96	1	VPR_HV1B4	P05945	human immun
8	10	50.0	96	1	VPR_HV1N5	P12540	human immun
9	10	50.0	96	1	VPR_HV1N5	P20941	human immun
10	10	50.0	96	1	VPR_HV1M1	P05944	human immun
11	10	50.0	96	1	VPR_HV1Z2	P12519	human immun
12	10	50.0	97	1	VPR_HV1A2	P05952	human immun
13	10	50.0	97	1	VPR_HV1Y2	P15067	human immun
14	8	40.0	96	1	VPR_HV1E1	P05946	human immun
15	8	40.0	96	1	VPR_HV1S1	P05951	human immun
16	8	40.0	65	1	VPR_HV1S1	P4672	eschwerichia
17	7	35.0	295	1	VPR_HV1S1	P05943	eschwerichia
18	7	35.0	459	1	VPR_HV1S1	P15162	eschwerichia
19	7	35.0	471	1	VPR_HV1S1	P29796	eschwerichia
20	7	35.0	647	1	VPR_HV1S1	P27282	eschwerichia
21	5	30.0	51	1	VPR_HV1S1	P27282	eschwerichia
22	5	30.0	64	1	VPR_HV1S1	P27282	eschwerichia
23	5	30.0	70	1	VPR_HV1S1	P27282	eschwerichia
24	5	30.0	125	1	VPR_HV1S1	P27282	eschwerichia
25	5	30.0	155	1	VPR_HV1S1	P27282	eschwerichia
26	5	30.0	155	1	VPR_HV1S1	P27282	eschwerichia
27	5	30.0	155	1	VPR_HV1S1	P27282	eschwerichia
28	5	30.0	155	1	VPR_HV1S1	P27282	eschwerichia
29	5	30.0	171	1	VPR_HV1S1	P27282	eschwerichia
30	5	30.0	171	1	VPR_HV1S1	P27282	eschwerichia
31	5	30.0	181	1	VPR_HV1S1	P27282	eschwerichia
32	5	30.0	181	1	VPR_HV1S1	P27282	eschwerichia
33	5	30.0	181	1	VPR_HV1S1	P27282	eschwerichia
34	5	30.0	181	1	VPR_HV1S1	P27282	eschwerichia

ALIGNMENTS

RESULT	1																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												</
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```

VR_HV1JR
ID VR_HV1JR STANDARD PRT 96 AA
AC P20883
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-JUL-1993 (Rel. 25, Last annotation update)
DE VPR PROTEIN (R ORF PROTEIN).
GN VPR.
OS Human immunodeficiency virus type 1 (T-cell isolate) (HIV-1).
OC Virus; Retroviridae; Lentivirinae; Lentivirus.
OX NCBI_TaxID:11688;
RN [1]
RP SEQUENCE FROM N.A.
RA Koyanagi S., Chen L.S.Y.
RL Submitted (DEC-1988) to the HIV data bank.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL: M38429; AB03747.1;
DR HIV: M38429; VPRJRGSP.
DR InterPro: IPR000012;
DR Pfam: PF00522; VPR_1
DR PRINTS: PR00444; HIVPRVPX
KW AIDS.
SQ
SEQUENCE 96 AA 11419 MW 6654572AEH2927 CP654;

Query Match
Best local Similarity 95.0% Score 19; FR 1; Length 96;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WLELELNKNEAVRHPR 20
ID 18 WLELELNKNEAVRHPR 36

RESULT 5
VR_HV1JM
ID VR_HV1JM STANDARD PRT 96 AA
AC P05950;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-JUL-1993 (Rel. 25, Last annotation update)
DE VPR PROTEIN (R ORF PROTEIN).
GN VPR.
OS Human immunodeficiency virus type 1 (MN isolate) (HIV-1).
OC Virus; Retroviridae; Lentivirinae; Lentivirus.
OX NCBI_TaxID:11688;
RN [1]
RP SEQUENCE FROM N.A.
RA Murphy R., Gao H.-G., Paredon G., Aldovini A., Collier R.,
RA Farrell K., Wong-Staal F., Gallo R.C., Potts M.S. Jr.;
RA "Envelope sequences of two new United States HIV-1 isolates."
RL Virology 164:531-536(1988).
RL -1- MISCELLANEOUS: THE MN ISOLATE WAS TAKEN FROM A PEDIATRIC AIDS
CC PATIENT IN 1984.
CC -----
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CC -----
DR EMBL: M17449; AAA44855.1;

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DR HIV: M17449; VPRSMN.
DR InterPro: IPR00012;
DR Pfam: PF00522; VPR_1.
DR PRINTS: PR00444; HIVPRVPX.
KW AIDS.
SQ
SEQUENCE 96 AA 11544 MW 27551LE237935E CP654;

Query Match
Best local Similarity 85.0% Score 17; FR 1; Length 96;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LLELELNKNEAVRHPR 20
ID 20 LLELELNKNEAVRHPR 36

RESULT 6
VR_HV1MC
ID VR_HV1MC STANDARD PRT 96 AA
AC P17287;
DT 01-NOV-1988 (Rel. 15, Created)
DT 01-DEC-1990 (Rel. 15, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE VPR PROTEIN (R ORF PROTEIN).
GN VPR.
OS Chimpanzee immunodeficiency virus (SIVcpz) (CIV).
OC Virus; Retroviridae; Lentivirinae; Lentivirus.
OX NCBI_TaxID:11723;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE:9025077; PubMed:2188136;
RA Hueb T., Cheynier P., Meyers R., Roelants G., Main-Hobson S.;
RA "Genetic organization of a chimpanzee lentivirus related to HIV-1."
RA Nature 345:355-359(1990).
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CC -----
DR EMBL: X52154; CAAC3403.1;
DR PIR: S09986; ASLJSC.
DR HIV: X52154; VPRSCPZ.
DR InterPro: IPR000012;
DR Pfam: PF00522; VPR_1.
DR PRINTS: PR00444; HIVPRVPX.
KW AIDS.
SQ
SEQUENCE 96 AA 11576 MW 16136544CDF3M3 CP654;

Query Match
Best local Similarity 70.0% Score 14; FR 1; Length 96;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLELELNKNEAVRHPR 20
ID 23 LLELELNKNEAVRHPR 36

RESULT 7
VR_HV1MA
ID VR_HV1MA STANDARD PRT 96 AA
AC P05950;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-JUL-1993 (Rel. 25, Last annotation update)
DE VPR PROTEIN (R ORF PROTEIN).
GN VPR.
OS Human immunodeficiency virus type 1 (MAL isolate) (HIV-1).

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[illegible]

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MATCHES          10:  CONSERVATIVE          0:  MISMATCHES          0:  INDELS          0:  GAPS          0:
OY      2 WTELELEER 11
      11111111
14.     13 WTELELEER 27

RESULT  9
VPR HIV10V
ID      VPR HIV10V          STANDARD:          PRT:          96 AA.
AC      P20801:
DE      01 FEB-1991 (Ref. 17, Cited)
DE      01 FEB-1991 (Ref. 17, Last sequence update)
DE      01-JUL-1993 (Ref. 26, Last annotation update)
DE      VPR PROTEIN (R ORF PROTEIN).
DE      VPR.
16      Human immunodeficiency virus type 1 (HTLV-1).
17      Viruses: Retroviral viruses; Retroviridae; Lentivirinae.
18      NC_011699:
19      11
20      SEQUENCE FROM N.A.
21      RX      MELLINE: 90148544: POPMOD:259749:
22      Host 1:  Dazza M.C., Brim-Welziet F., Roelants G.E., Main-Holston S.:
23      "A highly defective HIV-1 strain isolated from a healthy Caucasian
24      individual presenting an atypical western blot.",
25      AIDS 4:707-715(1990).
26      1  MISCELLANEOUS: THE OYT ISOLATE WAS TAKEN FROM THE HEAD OF A
27      HEALTHY CAINESE INDIVIDUAL.
28
29      THIS SWISS-PROT entry is copyright. It is produced through a collaboration
30      between the Swiss Institute of Bioinformatics and the EMBL outstation
31      at the European Bioinformatics Institute. There are no restrictions on the
32      use by non-profit institutions as long as its content is in no way
33      modified and this statement is not removed. Usage by and for commercial
34      entities requires a written agreement. For details see the file
35      or send an email to: license@isb.ch).
36
37      EMBL: M26727: AANA394.1:
38      HIV: M26727: VPR50Y1.
39      RefProt: PR0000127:
40      Pfam: PF00522: VPR:1.
41      PRINTS: PR00444: HIVVPRVX.
42      AIDS.
43      KW      SIGNATURE  96 AA: 11494 MW: 278084 IAE95482 CR664:
44
45      CDD: M26727: Score 10: BH 1: Length 96:
46      Best Local Similarity 100.0%: Pval. No. 0.0024:
47      Matches 10: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
48
49      OY      2 WTELELEER 11
50      11111111
51      13 WTELELEER 27

RESULT 10
VPR HIV10V
ID      VPR HIV10V          STANDARD:          PRT:          96 AA.
AC      P20904:
DE      01 MAY-1990 (Ref. 07, Cited)
DE      01 MAY-1990 (Ref. 07, Last sequence update)
DE      01-JUL-1993 (Ref. 26, Last annotation update)
DE      VPR PROTEIN (R ORF PROTEIN).
DE      VPR.
16      Human immunodeficiency virus type 1 (HTLV-1).
17      Viruses: Retroviral viruses; Retroviridae; Lentivirinae.
18      NC_011701:
19      11
20      SEQUENCE FROM N.A.
21      RX      Starich R.P., Rubin R.H., Shaw G.M., McNeely P.D., Motron S.,
22      Wolf H., Parks E.S., Parks W.F., Josephs S.F., Gallo R.C.:
23      "Wood Stalk P.:
24      Submitted (XXX-1987) to the HIV data bank.

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CC -----
DR EMBL: M17451; AAA45055.1; -
DR HIV: M17451; VPRSPF.
DR InterPro: IPR000612; -
DR Pfam: PF00522; VPR: 1.
DR PRINTS: PR00444; HIVPRVPX.
DR AIDS: -
SQ SEQUENCE 96 AA; 11389 MW; 676343D9579A944 CRC64;

Query Match 50.0%; Score 10; DB 1; Length 96;
Host Local Similarity 100.0%; Prod. No. 0.0024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 2 WTELELEIK 11
1111111111
DB 18 WTELELEIK 27

RESULT 11
VPR_HV122 STANDARD; PRT; 96 AA.
ID VPR_HV122 STANDARD; PRT; 96 AA.
AC P12519;
DI 01-OCT-1989 (rel 12, Created)
DI 01-OCT-1989 (rel 12, last sequence update)
DI 01-JUL-1994 (rel 26, last annotation update)
DE VPR PROTEIN (R ORF PROTEIN).
GN VPR.
OS Human immunodeficiency virus type 1 (Z270C/234 isolate) (HIV-1).
OC Viruses; Retroviruses; Retroviridae; Lentiviruses
OX NCBI_TaxID:11683;
RN [1]
RP SOURCE FROM N.A.
KA Theodore T. Buckler-White A.;
KL Submitted (MW-1988) to the HIV data bank.
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CC -----
DR EMBL: M22459; AAA45368.1; -
DR HIV: M22459; VPRSPF.
DR InterPro: IPR000612; -
DR Pfam: PF00522; VPR: 1.
DR PRINTS: PR00444; HIVPRVPX.
DR AIDS: -
SQ SEQUENCE 96 AA; 11389 MW; 65634D9579A944 CRC64;

Query Match 50.0%; Score 10; DB 1; Length 96;
Host Local Similarity 100.0%; Prod. No. 0.0024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 2 WTELELEIK 11
1111111111
DB 18 WTELELEIK 27

RESULT 11
VPR_HV122 STANDARD; PRT; 97 AA.
ID VPR_HV122 STANDARD; PRT; 97 AA.
AC P35967;
DI 01-JUN-1994 (rel 29, Created)
DI 01-JUN-1994 (rel 29, last sequence update)
DI 01-JUN-1994 (rel 29, last annotation update)
DE VPR PROTEIN (R ORF PROTEIN).
GN VPR.
OS Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).
OC Viruses; Retroviruses; Retroviridae; Lentiviruses.
OX NCBI_TaxID:36377;
RN [1]
RP SOURCE FROM N.A.
KA MEDLINE:9302187; PubMed:1404605;
KA Li Y., Hol E., Burgess C.J., Price R.W., Sharp P.M., Hahn B.H.,
KA Shaw G.M.;
RI *Complete nucleotide sequence, genome organization, and biological
RI properties of a new immunodeficiency virus (YU-2) in the AIDS
RI for limited detectiveness and complementation.*;
RI J. Virol. 66:6587-6600(1992).
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AC P05952;
DI 01-NOV-1988 (rel 09, Created)
DI 01-NOV-1988 (rel 09, last sequence update)
DI 01-JUL-1993 (rel 26, last annotation update)
DE VPR PROTEIN (R ORF PROTEIN).
GN VPR.
OS Human immunodeficiency virus type 1 (ARV-2) isolate (HIV-1).
OC Viruses; Retroviruses; Retroviridae; Lentiviruses.
OX NCBI_TaxID:11685;
RN [1]
RP SOURCE FROM N.A.
KA MEDLINE:8509454; PubMed:259927;
KA Sanchez-Pescador R., Power M.D., Barr P.J., Steiner K.S.,
KA Sanchez-Mon M., Brown-Shimer S.L., Lee W.W., Renard A., Randolph A.,
KA Levy J.A., Dina D., Luciw P.A.;
RI *Recombinant vaccine and expression of an AIDS-associated retrovirus
RI (ARV-2).";
RI J. Science 227:484-492(1985).
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CC -----
DR EMBL: K02007; AAG6478.1; -
DR HIV: K02007; VPRSPF2.
DR InterPro: IPR000612; -
DR Pfam: PF00522; VPR: 1.
DR PRINTS: PR00444; HIVPRVPX.
DR AIDS: -
SQ SEQUENCE 97 AA; 11557 MW; 49D49F62A932440 CRC64;

Query Match 50.0%; Score 10; DB 1; Length 97;
Host Local Similarity 100.0%; Prod. No. 0.0024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 2 WTELELEIK 11
1111111111
DB 18 WTELELEIK 27

RESULT 13
VPR_HV122 STANDARD; PRT; 97 AA.
ID VPR_HV122 STANDARD; PRT; 97 AA.
AC P35967;
DI 01-JUN-1994 (rel 29, Created)
DI 01-JUN-1994 (rel 29, last sequence update)
DI 01-JUN-1994 (rel 29, last annotation update)
DE VPR PROTEIN (R ORF PROTEIN).
GN VPR.
OS Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).
OC Viruses; Retroviruses; Retroviridae; Lentiviruses.
OX NCBI_TaxID:36377;
RN [1]
RP SOURCE FROM N.A.
KA MEDLINE:9302187; PubMed:1404605;
KA Li Y., Hol E., Burgess C.J., Price R.W., Sharp P.M., Hahn B.H.,
KA Shaw G.M.;
RI *Complete nucleotide sequence, genome organization, and biological
RI properties of a new immunodeficiency virus (YU-2) in the AIDS
RI for limited detectiveness and complementation.*;
RI J. Virol. 66:6587-6600(1992).
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Follet, Jane E. K.
REGISTRATION NUMBER: 33,342
PERFECTED/REGISTERED NUMBER: 0345,3106, 07008
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-965-58

Query Match 50.0% Score 13 DB 2 Length 13
Best Local Similarity 100.0% Pseq No. 1 20-07
Matches 13: Conservative 0 Mismatches 0 Indels 0 Caps 0

QY 10 LEHPRICGRSR 22
DB 1 LEHPRICGRSR 13

RESULT 5
US-08-484-965-58
Sequence 58, Application US/08481965H
Patent No. 6001146
GENERAL INFORMATION:
APPLICANT: Motiez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
TITLE OF INVENTION: Altered Major Histocompatibility Complex
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegun, Henderson, Parabow, Garrett &
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patonlin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09,421,965H
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,949
FILING DATE: 05-DEC-1994
CLASSIFICATION: 435
FEE: APPLICATION: N/A
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/REGISTERED NUMBER: 0345,3106, 07008
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 58:

SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-965-58

Query Match 50.0% Score 13 DB 3 Length 13
Best Local Similarity 100.0% Pseq No. 1 20-07
Matches 13: Conservative 0 Mismatches 0 Indels 0 Caps 0

QY 10 LEHPRICGRSR 22
DB 1 LEHPRICGRSR 13

RESULT 6
US-08-370-476-58
Sequence 58, Application US/08370476
Patent No. 6153408
GENERAL INFORMATION:
APPLICANT: Motiez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
APPLICANT: Lane, Yvonne
APPLICANT: Ojcius, David
APPLICANT: Castroue, Armand
TITLE OF INVENTION: Altered Major Histocompatibility Complex
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegun, Henderson, Parabow, Garrett &
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patonlin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,476
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117,575
FILING DATE: 07-SEP-1993
APPLICATION NUMBER: US 08/072,787
FILING DATE: 06-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/REGISTERED NUMBER: 0345,3106, 07008
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-370-476-58

Query Match 46.0% Score 14: 108 4: Length 14:
Post Local Similarity 100.0%: Prod. No. 1, 24-07:
Matches 14: Conservation 0: Mismatches 0: Indels 0: Gaps 0:

UY 3 BRIGOLLETHF 14
DB 1 BRIGOLLETHF 14

RESULT 7

US-09-001-915-4
Sequence 4: Application US/08-001-915

Patent No. 560,114

GENERAL INFORMATION:

APPLICANT: CHEN, Ette A.

APPLICANT: JEROME, Louis-Joe

APPLICANT: CHEN, Ette A.

APPLICANT: YAO, Xiao-Jian

APPLICANT: PONG-KO RONGER, Gary

TITLE OF INVENTION: PROTEIN TARGETING INTO HIV VIRIONS

TITLE OF INVENTION: BASED ON HIV-1 VPR FUSION MOLECULES

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: KLAIBER & JACKSON

STREET: Continental Plaza, 411 Backusack Avenue

CITY: Backusack

STATE: N.J.

COUNTRY: U.S.A.

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/001,915

FILING DATE:

CLASSIFICATION: C12

ATTORNEY/AGENT INFORMATION:

NAME: JACKSON, David A.

REGISTRATION NUMBER: 26,742

TITLE OF INVENTION: INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-487-5800

TELEX: 138521

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 72 amino acids

TYPE: amino acid

STANDARDIZATION: Single

Topography: Linear

MOLECULE TYPE: Protein

HYDROPHILIC: N

US-09-001-915-4

Query Match 46.0% Score 14: 108 4: Length 14:
Post Local Similarity 100.0%: Prod. No. 5, 50-05:
Matches 14: Conservation 0: Mismatches 0: Indels 0: Gaps 0:

UY 3 BRIGOLLETHF 14
DB 1 BRIGOLLETHF 14

RESULT 6

US-09-001-915-4
Sequence 4: Application US/08-001-915

Patent No. 560,114

GENERAL INFORMATION:

APPLICANT: CHEN, Ette A.

APPLICANT: JEROME, Louis-Joe

APPLICANT: CHEN, Ette A.

APPLICANT: YAO, Xiao-Jian

TITLE OF INVENTION: PROTEIN TARGETING INTO HIV VIRIONS

TITLE OF INVENTION: BASED ON HIV-1 VPR FUSION MOLECULES

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

APPLICANT: CHEN, Ette A.
APPLICANT: YAO, Xiao-Jian
APPLICANT: PONG-KO RONGER, Gary
TITLE OF INVENTION: PROTEIN TARGETING INTO HIV VIRIONS BASED
TITLE OF INVENTION: ON HIV-1 VPR FUSION MOLECULES

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: KLAIBER & JACKSON

STREET: Continental Plaza, 411 Backusack Avenue

CITY: Backusack

STATE: N.J.

COUNTRY: U.S.A.

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/001,915

FILING DATE: September 7, 1995

CLASSIFICATION: C12

ATTORNEY/AGENT INFORMATION:

NAME: JACKSON, David A.

REGISTRATION NUMBER: 26,742

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-487-5800

TELEX: 138521

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 72 amino acids

TYPE: amino acid

STANDARDIZATION: Single

Topography: Linear

MOLECULE TYPE: protein

HYDROPHILIC: NO

US-09-001-915-4

Query Match 46.2% Score 12: 108 3: Length 72:
Post Local Similarity 100.0%: Prod. No. 5, 50-05:
Matches 12: Conservation 0: Mismatches 0: Indels 0: Gaps 0:

UY 3 BRIGOLLETHF 14
DB 61 BRIGOLLETHF 72

RESULT 9

US-09-001-915-4
Sequence 5: Application US/09-001-915

Patent No. 5,268,484

GENERAL INFORMATION:

APPLICANT: KATINER, Hermann

APPLICANT: BOCHARTER, Andrea

APPLICANT: ERNST, Wolfgang

APPLICANT: BATTANI, Claudia

APPLICANT: PORTSCHER, Martin

APPLICANT: TREOLA, Alexandra

APPLICANT: BREDEL, Renate

APPLICANT: SCHMAIZ, Christine

APPLICANT: KLIMA, Andreas

APPLICANT: STEINIG, Frank

APPLICANT: MOTHER, Thomas

TITLE OF INVENTION: HIV Vaccines

FILE REFERENCE: 1989-11/16

CURRENT APPLICATION NUMBER: US/09/001,915

PRIOR APPLICATION NUMBER: DE/EP/95/01481

PRIOR FILING DATE: 1995-04-19

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patent in Version 3.0

SFO II No 5
LENGTH: 78
TYPE: PRT
ORGANISM: Human; Immunodeficiency virus type 1
US-09-124-900-5

Query Match 46.2% Score 12, PP 4, Length 78
Best Local Similarity 100.0%, Pred. No. 5, 9e-06,
Matches 12: Conservative 9; Mismatches 0; Indels 0; Gaps 0;

CY 14 FRICGHSR 14
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DB 61 FRICGHSR 72

RESULT 10
US-07-941-662-10
Sequence 30, Application US/07841662
Patent No. 5414413

GENERAL INFORMATION:
APPLICANT: Peterson, Per A
APPLICANT: Jackson, Michael
APPLICANT: Lenglade-Demoyen, Pierre
TITLE OF INVENTION: IN VITRO ACTIVATION OF CYTOTOXIC T CELLS
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:

ADDRESS: The Scripps Research Institute
STREET: 10556 No. 541441th Torrey Pines Road, TPO 8
CITY: La Jolla
STATE: California
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-07-941-662
FILING DATE: 19920219
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Logan, April
REGISTRATION NUMBER: 33,950
REFERENCE/DOCKET NUMBER: SPFO001P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 554-2937
TELEFAX: (619) 554-6312
INFORMATION FOR SFO ID NO: 30

SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
US-07-841-662-30

Query Match 24.6% Score 9, PP 1, Length 9;
Best Local Similarity 100.0%, Pred. No. 1, 5e-05;
Matches 9: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 14 FRICGHSR 22
|||||
DB 1 FRICGHSR 9

RESULT 11
US-08-209-797-30
Sequence 29, Application US/08209797
Patent No. 5529921

GENERAL INFORMATION:
APPLICANT: Peterson, Per A
APPLICANT: Jackson, Michael
APPLICANT: Lenglade-Demoyen, Pierre
TITLE OF INVENTION: IN VITRO ACTIVATION OF CYTOTOXIC T CELLS
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:

ADDRESS: The Scripps Research Institute
STREET: 10556 No. 5529921th Torrey Pines Road, TPO 8
CITY: La Jolla
STATE: California
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-08-209-797
FILING DATE: 10 MAR 1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US-07/841,662
FILING DATE: 19-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Logan, April
REGISTRATION NUMBER: 33,950

REFERENCE/DOCKET NUMBER: SPFO001P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 554-2937
TELEFAX: (619) 554-6312
INFORMATION FOR SFO ID NO: 30
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
US-08-209-797-30

Query Match 34.6% Score 9, PP 1, Length 9;
Best Local Similarity 100.0%, Pred. No. 1, 5e-05;
Matches 9: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 14 FRICGHSR 22
|||||
DB 1 FRICGHSR 9

RESULT 12
US-08-669-685-30
Sequence 30, Application US/08669685
Patent No. 5827737

GENERAL INFORMATION:
APPLICANT: Peterson, Per A
APPLICANT: Jackson, Michael
APPLICANT: Lenglade-Demoyen, Pierre
TITLE OF INVENTION: IN VITRO ACTIVATION OF CYTOTOXIC T CELLS
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:

ADDRESS: The Scripps Research Institute
STREET: 10556 No. 5827737th Torrey Pines Road, TPO 8
CITY: La Jolla

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1  STATE: California
2  COUNTRY: USA
3  ZIP: 92047
4  COMPUTER READABLE FORM:
5  MEDIUM TYPE: floppy disk
6  COMPUTER: IBM pc compatible
7  OPERATING SYSTEM: PC DOS/MS DOS
8  SOFTWARE: Patent in Release #1.0, Version #1.25
9  CURRENT APPLICATION DATA:
10 APPLICATION NUMBER: US/09/069,685
11 FILING DATE:
12 CLASSIFICATION: 435
13 PRIOR APPLICATION DATA:
14 APPLICATION NUMBER: US 09/209,797
15 FILING DATE: 16 MAR 1994
16 APPLICATION NUMBER: US 07/204,662
17 FILING DATE: 19 FEB 1992
18 ATTORNEY/AGENT INFORMATION:
19 NAME: Larson, April
20 REGISTRATION NUMBER: 34,950
21 REFERENCE/BOOKET NUMBER: SP0001P
22 TELECOMMUNICATION INFORMATION:
23 TELEPHONE: (419) 554-2947
24 TELEFAX: (419) 554-2947
25 INFORMATION FOR SEQ ID NO: 40:
26 SEQUENCE CHARACTERISTICS:
27 LENGTH: 9 amino acids
28 TYPE: amino acid
29 STRANDEDNESS: single
30 TOPOLOGY: linear
31 MODIFIABLE TYPE: peptide
32 HYDROPHOBIC: N
33 ANTI-SENSE: NO
34 FRAGMENT TYPE: Internal
35 ORIGIN: 655-40
36
37 Query Match 44.4% Score 92 DB 22 Length 92
38 Post Local Similarity 100.0% Ident. No. 1.5e+052
39 Matches 92 Conservative 02 Mismatches 02 Indels 02 Gaps 02
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41 14 FRAGMENT 22
42 11111111
43 1 FRAGMENT 9
44
45 RESULT 14
46 US-09-103-486-40
47 Sequence 40: Application US/09/069,685
48 Patent No. 6061545
49 GENERAL INFORMATION:
50 APPLICANT: Peterson, Peter A
51 APPLICANT: Jackson, Michael
52 APPLICANT: Longlake Biogen, Peter
53 TITLE OF INVENTION: IN VITRO ACTIVATION OF CYTOTOXIC T CELLS
54 NUMBER OF SEQUENCES: 40
55 CORRESPONDENCE ADDRESS:
56 ADDRESSEE: The Scripps Research Institute
57 STREET: 10550 No. 6004 604th Torrey Pines Road, Box 8
58 CITY: La Jolla
59 STATE: California
60 COUNTRY: USA
61 ZIP: 92037
62 COMPUTER READABLE FORM:
63 MEDIUM TYPE: floppy disk
64 COMPUTER: IBM pc compatible
65 OPERATING SYSTEM: PC DOS/MS DOS
66 SOFTWARE: Patent in Release #1.0, Version #1.25
67 CURRENT APPLICATION DATA:
68 APPLICATION NUMBER: US/09/103,486
69 FILING DATE:
70 CLASSIFICATION:
71 ANTI-SENSE:
72 FRAGMENT TYPE: Internal
73 PRIOR APPLICATION DATA:

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1  APPLICATION NUMBER: 09/069,685
2  FILING DATE:
3  APPLICATION NUMBER: US 07/841,662
4  FILING DATE: 19-FEB-1992
5  ATTORNEY/AGENT INFORMATION:
6  NAME: Larson, April
7  REGISTRATION NUMBER: 34,950
8  REFERENCE/BOOKET NUMBER: SP0001P
9  TELECOMMUNICATION INFORMATION:
10 TELEPHONE: (419) 554-2947
11 TELEFAX: (419) 554-6412
12 INFORMATION FOR SEQ ID NO: 40:
13 SEQUENCE CHARACTERISTICS:
14 LENGTH: 9 amino acids
15 TYPE: amino acid
16 STRANDEDNESS: single
17 TOPOLOGY: linear
18 MODIFIABLE TYPE: peptide
19 HYDROPHOBIC: N
20 ANTI-SENSE: NO
21 FRAGMENT TYPE: Internal
22 US-09-103-486-40

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1  Query Match 44.4% Score 92 DB 32 Length 92
2  Post Local Similarity 100.0% Ident. No. 1.5e+052
3  Matches 92 Conservative 02 Mismatches 02 Indels 02 Gaps 02
4
5  14 FRAGMENT 22
6  11111111
7  1 FRAGMENT 9
8
9  RESULT 14
10 US-09-039-982A-41
11 Sequence 41: Application US/09/099,982A
12 Patent No. 6225042
13 GENERAL INFORMATION:
14 APPLICANT: Cal, Zelig
15 APPLICANT: Sprent, Jonathan
16 APPLICANT: Brumback, Anders
17 APPLICANT: Jackson, Michael
18 APPLICANT: Peterson, Peter A
19 TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS FOR ACTIVATION OF T-C
20 NUMBER OF SEQUENCES: 59
21 CORRESPONDENCE ADDRESS:
22 ADDRESSEE: Olson & Hovl, Ltd.
23 STREET: 20 No. 6225042th Market Drive, Suite 3000
24 CITY: Chicago
25 STATE: Illinois
26 COUNTRY: USA
27 ZIP: 60606
28 COMPUTER READABLE FORM:
29 MEDIUM TYPE: floppy disk
30 COMPUTER: IBM pc compatible
31 OPERATING SYSTEM: PC DOS/MS-DOS
32 SOFTWARE: Patent in Release #1.0, Version #1.25
33 CURRENT APPLICATION DATA:
34 APPLICATION NUMBER: US/09/039,982A
35 FILING DATE: 16-MAR-1998
36 CLASSIFICATION: 435
37 ATTORNEY/AGENT INFORMATION:
38 NAME: Olson, Arno M.
39 REGISTRATION NUMBER: 40,204
40 REFERENCE/BOOKET NUMBER: ISK14710
41 TELECOMMUNICATION INFORMATION:
42 TELEPHONE: (412) 580-1186
43 TELEFAX: (412) 580-1189
44 INFORMATION FOR SEQ ID NO: 41:
45 SEQUENCE CHARACTERISTICS:
46 LENGTH: 9 amino acids
47 TYPE: amino acid
48 STRANDEDNESS: single

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? TOPOLOGY: linear
 ? MOLECULE TYPE: peptide
 ? HYPOTHETICAL: NO
 ? ANTI-STRIP: NO
 ? FRAGMENT TYPE: internal
 US-09-039-982A-41

Search completed: October 3, 2001, 13:25:46
 Job Time: 124 sec

Query Match 34.6%; Score 9; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.5e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FRIGCRHSR 22
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 DB 1 FRIGCRHSR 9

RESULT 15
 US-09-039-641-41
 : Sequence 41, Application US/09039641
 : Patent No. 6251627
 : GENERAL INFORMATION:
 : APPLICANT: Cal, Zelig
 : APPLICANT: Sprent, Jonathan
 : APPLICANT: Brumark, Anders
 : APPLICANT: Jackson, Michael
 : APPLICANT: Peterson, Per A
 : TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS FOR
 : TITLE OF INVENTION: ACTIVATION OF T-CELLS
 : NUMBER OF SEQUENCES: 45
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Olson & Hierl, Ltd.
 : STREET: 20 No. 6251627th Wacker Drive, Suite 3000
 : CITY: Chicago
 : STATE: Illinois
 : COUNTRY: USA
 : ZIP: 60606
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent Release #1 0, Version #1 25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/9/039,641
 : FILING DATE: 8-MAR-1995
 : CLASSIFICATION:
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Olson, Arne M.
 : REGISTRATION NUMBER: 30,203
 : REFERENCE/PACKET NUMBER: TSR14710
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (312) 580-1180
 : TELEFAX: (312) 580-1189
 : INFORMATION FOR SEQ ID NO. 41:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 9 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: peptide
 : HYPOTHETICAL: NO
 : ANTI-SENSE: NO
 : FRAGMENT TYPE: internal
 US-09-039-641-41

Query Match 34.6%; Score 9; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.5e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FRIGCRHSR 22
 |||||
 DB 1 FRIGCRHSR 9

Wed Oct 3 13:40:09 2001

us-09-485-421-1_copy_59_84.ra1

Page 8

GenBank version 1.5
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OM protein - protein search, using SW model

from: us-09-485-421-1_copy_59_84 (without alignments)
87,790 Million cell updates/sec

Title: US-09-485-421-1_copy_59_84

Perfect score: 26

Sequence: 1 ALPHILOLLEHFRHFCRHSRIGI 26

Scoring table: 61.100

Gapop: 60.0, Gapext: 60.0

Word size: 0

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

Database: PIP-68**

1: PIP1**
2: PIP2**
3: PIP3**
4: PIP4**

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	88.5	95	2	TPG383
2	19	69.2	95	2	SS4380
3	16	61.5	96	2	T09444
4	16	61.5	97	1	D44001
5	13	50.8	96	2	T01670
6	7	26.9	96	1	ASLJSC
7	7	26.9	356	2	T01435
8	7	26.9	356	2	T01498
9	7	26.9	357	2	T03920
10	7	26.9	357	2	T01434
11	7	26.9	461	2	SS5711
12	6	23.1	52	2	ASLJ32
13	6	23.1	87	2	H06753
14	6	23.1	89	2	S07691
15	6	23.1	92	2	S03067
16	6	23.1	98	2	B61369
17	6	23.1	101	1	ASLJ33
18	6	23.1	101	2	T11563
19	6	23.1	104	1	ASLJ34
20	6	23.1	105	1	ASLJ35
21	6	23.1	105	2	SS3095
22	6	23.1	122	1	ASLJ36
23	6	23.1	189	2	SS4502
24	6	23.1	213	2	SS4510
25	6	23.1	239	2	D64756
26	6	23.1	260	2	SS4945
27	6	23.1	284	2	SS4946
28	6	23.1	296	2	SS4947
29	6	23.1	305	2	AS5471

ALIGNMENTS

30 6 23.1 35 2 AS6354
31 6 23.1 34 2 T01434
32 6 23.1 37 2 T10247
33 6 23.1 38 2 B70544
34 6 23.1 40 2 F75341
35 6 23.1 43 2 AB3615
36 6 23.1 44 2 C96759
37 6 23.1 57 2 T10557
38 6 23.1 58 2 T14242
39 6 23.1 58 2 S17671
40 6 23.1 58 2 S41011
41 6 23.1 60 2 S54042
42 6 23.1 64 2 T25824
43 6 23.1 64 2 S41846
44 6 23.1 67 2 D85890
45 6 23.1 70 2 A45985

RESULTS

109383 vpr protein human immunodeficiency virus type 1 (isolate cnrl 1)

C:Species: human immunodeficiency virus type 1, HIV-1

A:Variety: isolate cnrl 1

C:Date: 11-Jun-1994 #seqname_revision 11 Jun-1994 #seq_change 21-hit-2000

C:Accession: T09383

R:Michael, N.L.; Chang, G.J.; d'Arcy, L.A.; Ehrenberg, P.K.; Mariani, R.; Busch, M.P.;

J. Virol. 69, 4028-4036, 1995

A:Title: Defective accessory genes in a human immunodeficiency virus type 1-infected

A:Reference number: 216654; M01D:95287175

A:Accession: T09383

A:Status: preliminary; translated from GP/PMH/DOB

A:Molecule type: DNA

A:Residues: 1-95 <MIC>

A:Cross-reference: EMBL:U04431; NID:920440; FIDN:AAA7077; PIP:q29443

C:Genetics:

A:Gene: vpr

C:Support family: AIDS vpr protein

C:Keywords: AIDS; immunodeficiency

Query Match 88.5% Score 23 DP 2 Length 95

Best Local Similarity 100.0% Prod. No. 5,20-17

Matches 23 Conservative 0 Mismatches 0 Indels 0 Gaps 0

DB 61 TRILLOLEHFRHFCRHSRIGI 83

SS4380

TPG383

SS4380

TPG383

Query Match 69.2% Score 19 DP 2 Length 96
Best Local Similarity 100.0% Prod. No. 7,60-12
Matches 19 Conservative 0 Mismatches 0 Indels 0 Gaps 0

A:Map position: 111,061-1
 A:Introns: 4371-15673, 17673-27613, 29113-39113
 C:Superfamily: dihydrokaempferol 4-reductase

Query Match 26.94, Score 7, E: 2, Length 357,
 Best Local Similarity 100.08, Pred. No. 5.3
 Matches 7, Conservative 0, Mismatches 0, Indels 0, Gaps 0

UY 4 R1000L 10
 |||||
 Db 241 R1000L 247

RESULT 8
 T01436
 NADPH HC-toxin reductase - maize
 C:Species: Zea mays (maize)
 A:Variety: inbred line MO21A
 C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 12-Nov-1999
 C:Accession: T01436
 R:Mitani, E.S., Moeley, E.B., Peterson, A.H., Gray, T., Rigney, S.P., Tobal, G.S.
 Proc. Natl. Acad. Sci. U.S.A. 95, 1686-1691, 1998
 A:Title: Plant pathogen microevolution: molecular basis for the origin of a fungal disease
 A:Reference number: 214328, PMID:98132652
 A:Accession: T01436
 A:Status: preliminary; translated from GH/EMBL/EMBL
 A:Molecule type: DNA
 A:Residues: 1-356 <MOL>
 A:Cross-references: PMID A001146, NID: g291157, FTK AAC0433, J. E. g291157
 A:Experimental source: inbred line MO21A
 A:Notes:
 A:Gene: hml
 A:Map position: 1
 A:Introns: 4371-15673, 17673-27613, 29113-39113
 C:Superfamily: dihydrokaempferol 4-reductase

Query Match 26.94, Score 7, E: 2, Length 357,
 Best Local Similarity 100.09, Pred. No. 5.3
 Matches 7, Conservative 0, Mismatches 0, Indels 0, Gaps 0

UY 4 R1000L 10
 |||||
 Db 241 R1000L 247

RESULT 9
 T03970
 NADPH HC-toxin reductase - maize
 C:Species: Zea mays (maize)
 C:Date: 22-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
 C:Accession: T03970
 R:Johal, G.S., Rigney, S.P.
 Science 258, 985-987, 1992
 A:Title: The hml disease resistance gene in maize encodes a reductase activity.
 A:Reference number: 215154, PMID:1306426
 A:Accession: T03970
 A:Status: preliminary; translated from CB/EMBL/EMBL
 A:Molecule type: DNA
 A:Residues: 1-357 <MOL>
 A:Cross-references: PMID 103540, NID: g15642, FTK AAC0433, J. E. g15643
 C:Genetics:
 A:Gene: hml
 C:Superfamily: dihydrokaempferol 4-reductase

Query Match 26.94, Score 7, E: 2, Length 357,
 Best Local Similarity 100.08, Pred. No. 5.3,
 Matches 7, Conservative 0, Mismatches 0, Indels 0, Gaps 0

UY 4 R1000L 10
 |||||

Db 241 R1000L 247

RESULT 10
 T01434
 NADH HC-toxin reductase hml maize
 C:Species: Zea mays (maize)
 C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 12-Nov-1999
 C:Accession: T01434
 R:Mitani, E.S., Moeley, E.B., Peterson, A.H., Gray, T., Rigney, S.P., Tobal, G.S.
 Proc. Natl. Acad. Sci. U.S.A. 95, 1686-1691, 1998
 A:Title: Plant pathogen microevolution: molecular basis for the origin of a fungal disease
 A:Reference number: 214328, PMID:98132652
 A:Accession: T01434
 A:Status: preliminary; translated from GH/EMBL/EMBL
 A:Molecule type: mRNA
 A:Residues: 1-357 <MOL>
 A:Cross-references: PMID A001146, NID: g291157, FTK AAC0433, J. E. g291158
 A:Experimental source: endosperm
 A:Notes:
 A:Gene: hml
 A:Map position: 111,061
 C:Superfamily: dihydrokaempferol 4-reductase

Query Match 26.94, Score 7, E: 2, Length 357,
 Best Local Similarity 100.08, Pred. No. 5.3
 Matches 7, Conservative 0, Mismatches 0, Indels 0, Gaps 0

UY 4 R1000L 10
 |||||
 Db 241 R1000L 247

RESULT 11
 S75711
 Hypothetical protein slr0866 - Synchocystis sp. (strain pvt 6803)
 C:Species: Synchocystis sp.
 A:Variety: pvt 6803
 C:Date: 25-Apr-1999 #sequence_revision 25-Apr-1999 #text_change 20-Jun-2000
 C:Accession: S75711
 R:Kaneko, T., Sato, S., Kotani, H., Tanaka, A., Asamizu, E., Nakamura, Y., Miyajima, O., K., Okumura, S., Shimpo, S., Takeuchi, C., Wada, T., Watanabe, A., Yamada, M., Yas
 DNA Res. 3, 109-116, 1996
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synchocystis
 S
 A:Reference number: S75711, PMID:97961201
 A:Accession: S75711
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-461 <MOL>
 A:Cross-references: PMID 10400, db Medline, NID: g1010, FTK PAA141, J. E. g1010
 A:Note: The nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C:Superfamily: conserved hypothetical protein H1612

Query Match 27.94, Score 7, E: 2, Length 461,
 Best Local Similarity 100.08, Pred. No. 6.6,
 Matches 7, Conservative 0, Mismatches 0, Indels 0, Gaps 0

UY 4 R1000L 10
 |||||
 Db 238 R1000L 244

RESULT 12
 A81042
 Hypothetical protein NM11795 (imported) Neisseria meningitidis (strain MC58 serogroup
 C:Species: Neisseria meningitidis
 C:Date: 01-Mar-2000 #sequence_revision 01-Mar-2000 #text_change 19-Jan-2001
 C:Accession: A81042
 R:Stettin, H., Sanders, N.J., Heideberg, J., Jeffries, A.C., Nelson, K.R., Eisen, R.
 Hickey, E.K., Haft, D.H., Salzberg, S.L., White, O., Fleischmann, R.D., Dougherty, B.

DE PARTIAL PROXIMAL VPR GENE (HML MNT ISOLATE) (FRAGMENT).
 GN Human immunodeficiency virus type 1
 GC Virusess; Retrovirda; Retrovirdae; Lentivirus.
 OX NCBI_TaxID:11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN HML MNT;
 RA Nakag K., Koopman D., Balliet J.W., Stijnvasan A., Collman R.G.;
 RT "Vsi-independent determinants of macrophage tropism in a primary human immunodeficiency virus type 1 isolate.";
 RL J. Virol. 69:1755-1761(1995).
 EH [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-89.6;
 RA MEDLINE:94059708; PubMed:1433527;
 RX Collman R., Balliet J.W., Gregory S.A., Friedman H., Koopman R.G.,
 RA Nathanson N., Stijnvasan A.;
 RT "An infectious molecular clone of an unusual macrophage-tropic and highly cytopathic strain of human immunodeficiency virus type 1.";
 RL J. Virol. 66:7517-7521(1992).
 DR EMBL: 039362; AAA81039.1; -;
 DR TRANSFAC: T02399; -;
 DR InterPro: IP000012; -;
 DR Pfam: PF00522; VPR; 1.
 DR PRINTS: PR00444; HIVPRVFX.
 SQ SEQUENCE 96 AA: 11516 MW: 042656544AFPEF CRG64;

Query Match 100.0%; Score 26; DB 14; Length 96;
 Best local similarity 100.0%; Prod. No. 2.4e-19;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATRTQGLLPFHRIGCRSRIGII 26
 DB 59 ATRTQGLLPFHRIGCRSRIGII 84

RESULT 3
 ID 07405 PRELIMINARY: PRT; 96 AA.
 AC 07405;
 DT 01-AUG-1998 (EMBLrel. 07, created)
 DT 01-AUG-1998 (EMBLrel. 07, last sequence update)
 DT 01-OCT-2000 (EMBLrel. 15, last annotation update)
 DE PARTIAL PROXIMAL VPR GENE (CHET_MNT ISOLATE) (FRAGMENT).
 GN VPR.
 OS Human immunodeficiency virus type 1.
 GC Virusess; Retrovirda; Retrovirdae; Lentivirus.
 OX NCBI_TaxID:11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN CHET_MNT;
 RA Nakag K., Koopman D., Compalin G., Patrick-Mathison P., Boussin F.,
 RA Moree D., Lastarrias G., Belmont D.;
 RT "Characterization of HIV-1 VPR, a proviral integrase, in the absence of integrase.";
 RL EMBL: Z82107; CAB0076.1; -;
 DR InterPro: IP000012; -;
 DR Pfam: PF00522; VPR; 1.
 DR PRINTS: PR00444; HIVPRVFX.
 FT NON_TER
 SQ SEQUENCE 96 AA: 11594 MW: 079504142AAHFF CRG64;

Query Match 100.0%; Score 26; DB 14; Length 96;
 Best local similarity 100.0%; Prod. No. 2.4e-19;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATRTQGLLPFHRIGCRSRIGII 26
 DB 59 ATRTQGLLPFHRIGCRSRIGII 84

RESULT 4
 ID 07469 PRELIMINARY: PRT; 96 AA.
 AC 07469;
 DT 01-NOV-1996 (EMBLrel. 01, created)
 DT 01-NOV-1996 (EMBLrel. 01, last sequence update)
 DT 01-MAY-2000 (EMBLrel. 15, last annotation update)
 DE VPR PROTEIN.
 GN VPR.
 OS Human immunodeficiency virus type 1.

GC Virusess; Retrovirda; Retrovirdae; Lentivirus.
 OX NCBI_TaxID:11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-89.6;
 RX MEDLINE:95156606; PubMed:7854514;
 RA Kim P.M., Koopman D., Balliet J.W., Stijnvasan A., Collman R.G.;
 RT "Vsi-independent determinants of macrophage tropism in a primary human immunodeficiency virus type 1 isolate.";
 RL J. Virol. 69:1755-1761(1995).
 EH [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-89.6;
 RA MEDLINE:94059708; PubMed:1433527;
 RX Collman R., Balliet J.W., Gregory S.A., Friedman H., Koopman R.G.,
 RA Nathanson N., Stijnvasan A.;
 RT "An infectious molecular clone of an unusual macrophage-tropic and highly cytopathic strain of human immunodeficiency virus type 1.";
 RL J. Virol. 66:7517-7521(1992).
 DR EMBL: 039362; AAA81039.1; -;
 DR TRANSFAC: T02399; -;
 DR InterPro: IP000012; -;
 DR Pfam: PF00522; VPR; 1.
 DR PRINTS: PR00444; HIVPRVFX.
 SQ SEQUENCE 96 AA: 11395 MW: 223807934DEF238 CRG64;

Query Match 100.0%; Score 26; DB 14; Length 96;
 Best local similarity 100.0%; Prod. No. 2.4e-19;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATRTQGLLPFHRIGCRSRIGII 26
 DB 59 ATRTQGLLPFHRIGCRSRIGII 84

RESULT 5
 ID 09E248 PRELIMINARY: PRT; 96 AA.
 AC 09E248;
 DT 01-MAR-2001 (EMBLrel. 16, created)
 DT 01-MAR-2001 (EMBLrel. 16, last sequence update)
 DT 01-MAR-2001 (EMBLrel. 16, last annotation update)
 DE VPR PROTEIN (FRAGMENT).
 GN VPR.
 OS Human immunodeficiency virus type 1.
 GC Virusess; Retrovirda; Retrovirdae; Lentivirus.
 OX NCBI_TaxID:11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MNT4.2;
 RA Ahmed N., Vedaivalil V.S.R.K.;
 RT "Low Conservation of Functional Domains of Human Immunodeficiency Virus Type 1 Vif and Vpr Genes Correlates with Lack of Vertical Transmission.";
 RL Submitted (2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF275119; AA332277.1; -;
 FT NON_TER
 SQ SEQUENCE 96 AA: 11398 MW: 0680962875196810 CRG64;

Query Match 100.0%; Score 26; DB 14; Length 96;
 Best local similarity 100.0%; Prod. No. 2.4e-19;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATRTQGLLPFHRIGCRSRIGII 26
 DB 59 ATRTQGLLPFHRIGCRSRIGII 84

RESULT 6
 ID 09E247 PRELIMINARY: PRT; 96 AA.

```

AC 09E247:
DI 01-MAR-2001 (TRENBLER, 16, Created)
DI 01-MAR-2001 (TRENBLER, 16, Last sequence update)
DI 01-MAR-2001 (TRENBLER, 16, Last annotation update)
DE VPR PROTEIN (FRAGMENT).
GN VPR.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentiviruses.
OX NCBI_TaxID:11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN MT4.3;
KA Ahmad N., Yodaishi V.S.R.K.;
KT "Low Conservation of Functional Domains of Human Immunodeficiency
RT Virus Type 1 vif and vpr Genes Correlates with Lack of Vertical
RT Transmission."
RL Submitted (JUN-2000) to the EMBL/Genbank/JFRRJ databases.
DR EMBL: AF275129; AAC32276.1;
FT NON-TER
FT SEQUENCE 96 AA: 11368 MW: 068990275196810 CRC64;
SQ

```

```

Query Match 100.0%; Score 26; DI 14; Length 96;
Best Local Similarity 100.0%; Pred. No. 2.4e-19;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 ALIRLQQLFHFPRIGCRHSRIGI 26
DI 59 ALIRLQQLFHFPRIGCRHSRIGI 84

```

```

RESULT 7
Q9E246 PRELIMINARY: PRT; 96 AA.
DI 01-MAR-2001 (TRENBLER, 16, Created)
DI 01-MAR-2001 (TRENBLER, 16, Last sequence update)
DI 01-MAR-2001 (TRENBLER, 16, Last annotation update)
DE VPR PROTEIN (FRAGMENT).
GN VPR.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentiviruses.
OX NCBI_TaxID:11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN MT4.3;
KA Ahmad N., Yodaishi V.S.R.K.;
KT "Low Conservation of Functional Domains of Human Immunodeficiency
RT Virus Type 1 vif and vpr Genes Correlates with Lack of Vertical
RT Transmission."
RL Submitted (JUN-2000) to the EMBL/Genbank/JFRRJ databases.
DR EMBL: AF275129; AAC32276.1;
FT NON-TER
FT SEQUENCE 96 AA: 11368 MW: 068990275196810 CRC64;
SQ

```

```

Query Match 100.0%; Score 26; DI 14; Length 96;
Best Local Similarity 100.0%; Pred. No. 2.4e-19;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 ALIRLQQLFHFPRIGCRHSRIGI 26
DI 59 ALIRLQQLFHFPRIGCRHSRIGI 84

```

```

RESULT 8
Q9E245 PRELIMINARY: PRT; 96 AA.
DI 01-MAR-2001 (TRENBLER, 16, Created)
DI 01-MAR-2001 (TRENBLER, 16, Last sequence update)
DI 01-MAR-2001 (TRENBLER, 16, Last annotation update)
DE VPR PROTEIN (FRAGMENT).

```

```

GN VPR.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentiviruses.
OX NCBI_TaxID:11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MT4.3;
KA Ahmad N., Yodaishi V.S.R.K.;
KT "Low Conservation of Functional Domains of Human Immunodeficiency
RT Virus Type 1 vif and vpr Genes Correlates with Lack of Vertical
RT Transmission."
RL Submitted (JUN-2000) to the EMBL/Genbank/JFRRJ databases.
DR EMBL: AF275129; AAC32280.1;
FT NON-TER
FT SEQUENCE 96 AA: 11368 MW: 068990275196810 CRC64;
SQ

```

```

Query Match 100.0%; Score 26; DI 14; Length 96;
Best Local Similarity 100.0%; Pred. No. 2.4e-19;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 ALIRLQQLFHFPRIGCRHSRIGI 26
DI 59 ALIRLQQLFHFPRIGCRHSRIGI 84

```

```

RESULT 9
Q9E244 PRELIMINARY: PRT; 96 AA.
DI 01-MAR-2001 (TRENBLER, 16, Created)
DI 01-MAR-2001 (TRENBLER, 16, Last sequence update)
DI 01-MAR-2001 (TRENBLER, 16, Last annotation update)
DE VPR PROTEIN (FRAGMENT).
GN VPR.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentiviruses.
OX NCBI_TaxID:11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MT4.3;
KA Ahmad N., Yodaishi V.S.R.K.;
KT "Low Conservation of Functional Domains of Human Immunodeficiency
RT Virus Type 1 vif and vpr Genes Correlates with Lack of Vertical
RT Transmission."
RL Submitted (JUN-2000) to the EMBL/Genbank/JFRRJ databases.
DR EMBL: AF275129; AAC32281.1;
FT NON-TER
FT SEQUENCE 96 AA: 11368 MW: 068990275196810 CRC64;
SQ

```

```

Query Match 100.0%; Score 26; DI 14; Length 96;
Best Local Similarity 100.0%; Pred. No. 2.4e-19;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 ALIRLQQLFHFPRIGCRHSRIGI 26
DI 59 ALIRLQQLFHFPRIGCRHSRIGI 84

```

```

RESULT 10
Q9E243 PRELIMINARY: PRT; 96 AA.
DI 01-MAR-2001 (TRENBLER, 16, Created)
DI 01-MAR-2001 (TRENBLER, 16, Last sequence update)
DI 01-MAR-2001 (TRENBLER, 16, Last annotation update)
DE VPR PROTEIN (FRAGMENT).
GN VPR.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentiviruses.
OX NCBI_TaxID:11676;
RN [1]

```

```

RP SEQUENCE FROM N.A.
RC STRAIN MN4.12
RA Ahmad N., Yoshida H., V.S.P.K.:
RI "Low conservation of functional domains of Human Immunodeficiency
RT Virus Type 1 vit and vpr genes correlates with lack of vertical
R1 transmission."
R2 Submitted (JUN 2000) to the EMBL/GenBank/CCDB databases.
RC EMBL: AF275124; AM54286.1;
RT NON-TER
SI SEQUENCE 96 AA: 11588 MW: 6680938751.06810 CRO744;

Query Match
Best Local Similarity 100.0% Score 26; DB 14; Length 96;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALTRLDQGLFTHPRIGRHSRI11 26
ID 59 ALTRLDQGLFTHPRIGRHSRI11 84
AC G9E241; PRELIMINARY; PRT; 96 AA.
DT 01-MAR-2001 (EMBLrel. 16, created)
DT 01-MAR-2001 (EMBLrel. 16, last sequence update)
DT 01-MAR-2001 (EMBLrel. 16, last annotation update)
DE VPR PROTEIN (FRAGMENT).
GN VPR.
OS Human Immunodeficiency Virus Type 1.
OC Viruses; Retroviruses; Retroviridae; Lentiviruses.
CX NCBI TaxID 11676;
LN 11
RC SEQUENCE FROM N.A.
RA Ahmad N., Yoshida H., V.S.P.K.:
RI "Low conservation of functional domains of Human Immunodeficiency
RT Virus Type 1 vit and vpr genes correlates with lack of vertical
R1 transmission."
R2 Submitted (JUN 2000) to the EMBL/GenBank/CCDB databases.
RC EMBL: AF275124; AM54286.1;
RT NON-TER
SI SEQUENCE 96 AA: 11588 MW: 6680938751.06810 CRO744;

Query Match
Best Local Similarity 100.0% Score 26; DB 14; Length 96;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALTRLDQGLFTHPRIGRHSRI11 26
ID 59 ALTRLDQGLFTHPRIGRHSRI11 84
AC G9E241; PRELIMINARY; PRT; 96 AA.
DT 01-MAR-2001 (EMBLrel. 16, created)
DT 01-MAR-2001 (EMBLrel. 16, last sequence update)
DT 01-MAR-2001 (EMBLrel. 16, last annotation update)
DE VPR PROTEIN (FRAGMENT).
GN VPR.
OS Human Immunodeficiency Virus Type 1.
OC Viruses; Retroviruses; Retroviridae; Lentiviruses.
CX NCBI TaxID 11676;
LN 11
RC SEQUENCE FROM N.A.
RA Ahmad N., Yoshida H., V.S.P.K.:
RI "Low conservation of functional domains of Human Immunodeficiency
RT Virus Type 1 vit and vpr genes correlates with lack of vertical
R1 transmission."
R2 Submitted (JUN 2000) to the EMBL/GenBank/CCDB databases.
RC EMBL: AF275124; AM54286.1;
RT NON-TER
SI SEQUENCE 96 AA: 11588 MW: 6680938751.06810 CRO744;

```

```

RT TRANSMISSION."
R2 Submitted (JUN 2000) to the EMBL/GenBank/CCDB databases.
RC EMBL: AF275124; AM54286.1;
RT NON-TER
SI SEQUENCE 96 AA: 11588 MW: 6680938751.06810 CRO744;

Query Match
Best Local Similarity 100.0% Score 26; DB 14; Length 96;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALTRLDQGLFTHPRIGRHSRI11 26
ID 59 ALTRLDQGLFTHPRIGRHSRI11 84
AC G9E249; PRELIMINARY; PRT; 96 AA.
DT 01-MAR-2001 (EMBLrel. 16, created)
DT 01-MAR-2001 (EMBLrel. 16, last sequence update)
DT 01-MAR-2001 (EMBLrel. 16, last annotation update)
DE VPR PROTEIN (FRAGMENT).
GN VPR.
OS Human Immunodeficiency Virus Type 1.
OC Viruses; Retroviruses; Retroviridae; Lentiviruses.
CX NCBI TaxID 11676;
LN 11
RC SEQUENCE FROM N.A.
RA Ahmad N., Yoshida H., V.S.P.K.:
RI "Low conservation of functional domains of Human Immunodeficiency
RT Virus Type 1 vit and vpr genes correlates with lack of vertical
R1 transmission."
R2 Submitted (JUN 2000) to the EMBL/GenBank/CCDB databases.
RC EMBL: AF275129; AM54286.1;
RT NON-TER
SI SEQUENCE 96 AA: 11588 MW: 6680938751.06810 CRO744;

Query Match
Best Local Similarity 100.0% Score 26; DB 14; Length 96;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALTRLDQGLFTHPRIGRHSRI11 26
ID 59 ALTRLDQGLFTHPRIGRHSRI11 84
AC G9E253; PRELIMINARY; PRT; 96 AA.
DT 01-NOV-1996 (EMBLrel. 01, created)
DT 01-NOV-1996 (EMBLrel. 01, last sequence update)
DT 01-MAY-2000 (EMBLrel. 13, last annotation update)
DE VPR PROTEIN.
GN VPR.
OS Human Immunodeficiency Virus Type 1.
OC Viruses; Retroviruses; Retroviridae; Lentiviruses.
CX NCBI TaxID 11676;
LN 11
RC SEQUENCE FROM N.A.
RA STRAIN PATIENT 4497, HOMOSEXUAL, GERMANY.
RA KATKEE L., GORDON-LEITCH E., ZWISLOCKY F., HARTMAN C., CHIBBS J.,
RA GORDON L.:
R2 J. Gen. Virol. 0:0-0(1996).
RC EMBL: Z68567; CAA92861.1;
DE IndetPro: IP000012;
DE P1am: PF06722; VPR: 1;
DE PRIN1: PR00444; HIVPRVFX;
SI SEQUENCE 94 AA: 11558 MW: 6285794201.280720 CRO744;

```


1

2

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OR protein protein search, using sw method

Run on: October 3, 2001, 13:38:32, Search time: 13.68 seconds
(without alignments)
65,105 Million cell updates/sec

Title: US 09 485 421-1_COPY_59_84

Perfect score: 26

Sequence: 1 ALIRLQQLLFTFRIGCHSRIGII 26

Scoring table:

Gapop 60.0, Gapext 60.0

Searched: 93435 seqs, 34255486 residues

Word size: 6

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database: SWISSPROT_39*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	92.3	96	1	VPR_HV1MN
2	24	92.3	96	1	VPR_HV1SC
3	23	84.6	96	1	VPR_HV1JP
4	22	84.6	96	1	VPR_HV1RP
5	22	84.6	96	1	VPR_HV1RS
6	18	65.2	96	1	VPR_HV1R2
7	16	61.5	96	1	VPR_HV1EL
8	16	61.5	96	1	VPR_HV1OY
9	16	61.5	96	1	VPR_HV1H
10	16	61.5	96	1	VPR_HV1A2
11	16	61.5	96	1	VPR_HV1A3
12	13	50.0	96	1	VPR_HV1MA
13	12	45.2	78	1	VPR_HV1BI
14	12	45.2	78	1	VPR_HV1B5
15	8	30.8	101	1	VPR_SIVSP
16	7	26.9	96	1	VPR_SIVSZ
17	7	26.9	96	1	VPR_SIVS3
18	6	23.1	89	1	VPR_SIVS4
19	6	23.1	87	1	VPR_SIVWK
20	6	23.1	101	1	VPR_SIVKI
21	6	23.1	104	1	VPR_HV2ST
22	6	23.1	105	1	VPR_HV2D1
23	6	23.1	105	1	VPR_HV2D2
24	6	23.1	122	1	VPR_SIVWL
25	6	23.1	212	1	HISB_MVCEM
26	6	23.1	219	1	VPR_SIVKT
27	6	23.1	220	1	VPR_SIVKT
28	6	23.1	242	1	VPR_SIVKT
29	6	23.1	242	1	VPR_SIVKT
30	6	23.1	353	1	CKPR_MORSE
31	6	23.1	379	1	CKPR_MORSE
32	6	23.1	389	1	HISB_MVCEM
33	6	23.1	394	1	KTRF_PAT

34	6	23.1	589	1	Y041_CAERL
35	6	23.1	634	1	Y041_CAERL
36	6	23.1	704	1	H001_PABIT
37	6	23.1	704	1	H001_PABIT
38	6	23.1	704	1	NEUL_PABIT
39	6	23.1	778	1	NEUL_PABIT
40	6	23.1	802	1	P001_MOUSE
41	6	23.1	906	1	AMPD_HUMAN
42	6	23.1	1016	1	AMPD_HUMAN
43	6	23.1	1091	1	AMPD_HUMAN
44	6	23.1	1091	1	AMPD_HUMAN
45	6	23.1	1314	1	V171_HUMAN

ALIGNMENTS

RESULT 1

VPR_HV1MN STANDARD: PRT: 96 AA.

AC P05950:

DT 01-NOV-1988 (Rel. 09, Created)

DT 01-NOV-1988 (Rel. 09, Last sequence update)

DE 01-JUL-1993 (Rel. 26, Last annotation update)

DE VPR PROTEIN (R ORF PROTEIN).

GN VPR.

OS Human immunodeficiency virus type 1 (MN isolate) (HIV-1).

OX Viruses; Retroviral viruses; Retroviridae; Lentivirus.

RN NCBI_TaxID=11696;

RP SEQUENCE FROM N.A.

FA Gougo C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,

FA Farrelly K., Wang S.-L., Salas R., Kelly M.S., Jr.,

RT "Envelope sequences of two new United States HIV-1 isolates."

CC Virology 164:531-536(1988).

CC -1- MISCELLANEOUS: THE MN ISOLATE WAS TAKEN FROM A PATIENT IN 1984.

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Query Match: 92.3%, Score 24, 25 L, Length 96,
Best local similarity: 100.0%, Pred. NO. left: 0;
Matches: 24; Conservative: 0; Mismatches: 0; Indels: 0;
Gaps: 0;

3 TRILQQLLFTFRIGCHSRIGII 26
|||||
61 TRILQQLLFTFRIGCHSRIGII 84

RESULT 2
VPR_HV1SC STANDARD: PRT: 96 AA.
AC P05951:
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DE 01-JUL-1993 (Rel. 26, Last annotation update)
DE VPR PROTEIN (R ORF PROTEIN).


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05 Human immunodeficiency virus type 1 (New York-5 isolate) (HIV-1).
06 Viruses: Retroviral viruses; Retroviridae; Lentivirus.
07 NCBI_TaxID:11698;
08 [1]
09
10 SEQUENCE FROM N.A.
11 Buckner G.F., Buckner-White A.J., Willey R.L., McCoy J.J.
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